



### SEQUENCE LISTING

<110> Kalyanaraman Ramnarayan Edward T. Maggio P. Patrick Hess

<120> Use of Computationally Derived Protein Structures of Genetic Polymorphisms in Pharmacogenomics for Drug Design and Clinical Applications RECEIVED

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TECH CENTER 1600/2900

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ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta
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Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
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tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata
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Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
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Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
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Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
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caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta
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Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Val Lys Ile Gly
                                                                               48
ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta
                                                                               96
Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg
                                                                              144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
                                                                              192
gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca
                                                                              240
Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr
cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
                                                                              288
                                                                              336
tta aat ttt cct att aqt cct att qaa act gta cca gta aaa tta aag
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                                                                              384
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
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aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg
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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                                                                              480
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc
                                                                              528
Ala Ile Lys Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe
                                                                              576
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                                           190
             180
                                                                              624
ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
                                                                              672
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
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                                                 220
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aag Lys 225	${ t Tyr}$	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
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gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
agc Ser	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	cta Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	tta Leu	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
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gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
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gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aag Lys 265	atc Ile	tta Leu	gar Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
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gga tcw gac tta gaa ata ggg caa cat aga ata aaa ata gag gaa ctg Gly Xaa Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu 290 295 300	912
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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atw ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240

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cca Pro	gga Gly	atg Met	gat Asp 115	ggc Gly	cca Pro	aga Arg	gtt Val	aaa Lys 120	caa Gln	tgg Trp	cca Pro	ttg Leu	aca Thr 125	gaa Glu	gaa Glu	384
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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata gtg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
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cag aaa gaa Gln Lys Glu	cct cca t Pro Pro P 325	tc ctt t he Leu T	Trp Met	ggc tat Gly Tyr 330	gaa ct Glu Le	c cat u His	cct Pro 335	gat Asp	1008
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cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttt Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
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Gly (	caa Gln	cta a Leu 1	arg o Xaa 0 20	gaa g Blu <i>P</i>	gct d Ala I	cta a Leu I	ata q [le ]	gat a Asp 1 25	aca q Thr (	gga q Gly i	gca g Ala i	gat g Asp i	gat Asp 30	aca Thr	gta Val	96

tta Leu	gaa Glu	gac Asp 35	ata Ile	gat Asp	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aga Arg	cca Pro	aga Arg 45	atg Met	ata Ile	Gly ggg	144
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		cat His														960
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gto Va	c aat L Asr	gad n Asp 355	o Ile	a caa e Glr	a aag n Lys	g tta G Leu	gtg Val	. Gly	a aaa ⁄ Lys	tta Lev	a aat 1 Asr	tgg Trp 365	) Ala	a agt a Ser	cag Gln	1104
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gly ggg	caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
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Gly 999	caa Gln	cta Leu	aag Lys 20	gag Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96 144
gta gaa gaa atg aat tta tca gga agg tgg aaa cca aaa atg ata ggg Val Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly	
gta gaa gaa atg aat tta tca gga agg tgg aaa cca aaa atg ata ggg Val Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly 35  gga att gga ggt ttt atc aaa gta aga saa tat gaa cag ata cct gta Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Glu Gln Ile Pro Val	144

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cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	ccg Pro	aga Arg	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	Thr	gaa Glu	gaa Glu	384
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gto Val	aat L Asr	gac Asp 355	) Ile	caa Glr	a aaa n Lys	gtt Val	agt Ser 360	Gly	aaa Lys	att : Ile	aaa Lys	tto Leu 365	ı Gly	aag Lys	g tca Ser	1104
		ı Pro	agg Arg													1117
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Gly 999	caa Gln	cta Leu	acg Thr 20	gaa Glu	gct Ala	yta Xaa	ttg Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	aat Asn 30	aca Thr	gta Val	96
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cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	gat Asp	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
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 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
tta gaa gac ata aat ttg cca ggg aaa tgg aaa cca aaa atg ata qqq
                                                                                 144
Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
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Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val
gaa att tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca
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Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr
cct gtc aac gta att gga aga aat ctg atg act cag att ggc tgc act
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Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca tta aca gaa gaa
                                                                                 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
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aaa ata aaa gca tta gta gaa att tgc aca gaa ttg gaa aag gaa ggg
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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
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                                                                                 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
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                                               155
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Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
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Gly 999	caa Gln	cta Leu	aaa Lys 20	gaa Glu .	gct Ala	cta Leu	tta Leu	gay Asp 25	aca Thr	ggg Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96

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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

gcy at Xaa Il	a cac e His	aag Lys	aaa Lys 165	Asn	agt Ser	aat Asn	aga Arg	tgg Trp 170	aga Arg	aaa Lys	gta Val	gta Val	gat Asp 175	Phe	528
agg ga Arg Gl	a ctt u Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata co Ile Pr	a cat o His 195	Pro	gca Ala	gga Gly	tta Leu	aaa Lys 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat gt Asp Va 21	l Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aag Lys	gat Asp	ttc Phe	agg Arg	672
aag ta Lys Ty 225	t act r Thr	gcg Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
atc ag Ile Ar	a tac g Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca at Ala Il	a ttc e Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aga Arg 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa aa Gln As	t cca n Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga to Gly Se 29	r Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	aak Xaa	gaa Glu	ctg Leu	912
aga saa Arg Xaa 305	a cat a His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	ttc Phe	aca Thr 315	cca Pro	gac Asp	caa Gln	aaa Lys	cat His 320	960
cag aaa Gln Ly:	a gaa s Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa tgg Lys Tr	g aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aar Lys	gac Asp	agt Ser 350	tgg Trp	acw Xaa	1056
gty aat Xaa Asr	gac Asp 355	ata Ile	cag Gln	aaa Lys	tta Leu	gtk Xaa 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	caa Gln	1104
att tad Ile Tyr 370	Pro														1116
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aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 235 230 235 240	720
atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu 290 295 300	912
aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa 340 345 350	1056
gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg caa cta aag gaa gct cta cta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96

tta Leu	gaa Glu	gaa Glu 35	atg Met	agt Ser	ttg Leu	cca Pro	gga Gly 40	aaa Lys	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	gly ggg	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	gta Val	tcc Ser	atg Met	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gtt Val	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	tct Ser	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ytg Xaa	ttg Leu 90	act Thr	cag Gln	ctt Leu	Gly 999	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	ata Ile	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gar Glu	Gly ggg	432
												act Thr				480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aag Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aaa Lys	act Thr	caa Gln	gat Asp 185	ttc Phe	tgg Trp	gaa Glu	rtt Xaa	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly aaa	tta Leu	caa Gln 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtc Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	Phe	caa Gln 260	tat Tyr	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	Ile	tac Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 60	192
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240

tta Leu	aat Asn	ttt Phe	cct Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aaa Lys	336
								aaa Lys								384
								tgt Cys								432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	ata Ile	ttt Phe 160	480
								aga Arg								528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gat Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
								aag Lys								624
								gtt Val								672
								agt Ser								720
								cca Pro								768
								aaa Lys 265								816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	cag Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
								cat His								912
								ttt Phe								960
cag Gln	aaa Lys	gaa Glu	cct Pro	ccm Xaa 325	ttc Phe	cak Xaa	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cay His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cas Xaa	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gat Asp	agc Ser 350	tgg Trp	act Thr	1056

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104													
att tac cca ggg Ile Tyr Pro Gly 370	1116													
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96													
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly 35 40 45	144													
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192													
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240													
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288													
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336													
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384													
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gcc Ala	ata Ile	aag Lys	aag Lys	aaa Lys 165	Ser	ggt Gly	aga Arg	tgg Trp	aga Arg 170	Lys	ata Ile	gta Val	gat Asp	ttt Phe	aga Arg	52	8
gaa Glu	ctt Leu	aat Asn	aag Lys 180	aga Arg	act Thr	caa Gln	gat Asp	ttc Phe 185	Trp	gaa Glu	gtt Val	caa Gln	tta Leu 190	. Gly	ata Ile	57	6
cca Pro	cat His	ccc Pro 195	Ala	gly aaa	tta Leu	aaa Lys	aag Lys 200	aac Asn	aag Lys	tca Ser	gta Val	aca Thr 205	Ile	ctg Leu	gat Asp	62	4
gtg Val	ggt Gly 210	gat Asp	gca Ala	tat Tyr	ttt Phe	tca Ser 215	gtt Val	ccc Pro	tta Leu	gat Asp	aag Lys 220	gaa Glu	ttc Phe	agg Arg	aag Lys	67	2
tat Tyr 225	act Thr	gca Ala	ttt Phe	acc Thr	ata Ile 230	cct Pro	agt Ser	ata Ile	aat Asn	aat Asn 235	gag Glu	aca Thr	cca Pro	gly ggg	att Ile 240	72	0
aga Arg	tat Tyr	cag Gln	tac Tyr	aat Asn 245	gtg Val	ctt Leu	cca Pro	cag Gln	gga Gly 250	tgg Trp	aaa Lys	gga Gly	tca Ser	cca Pro 255	gca Ala	76	8
ata Ile	ttc Phe	caa Gln	agt Ser 260	agc Ser	atg Met	aca Thr	aaa Lys	atc Ile 265	tta Leu	gag Glu	cct Pro	ttt Phe	aga Arg 270	aaa Lys	caa Gln	810	5
aat Asn	cca Pro	gac Asp 275	ata Ile	gtt Val	atc Ile	tat Tyr	cag Gln 280	tac Tyr	gtg Val	gat Asp	gat Asp	ttg Leu 285	tat Tyr	gta Val	gga Gly	864	1
tct Ser	gat Asp 290	tta Leu	gaa Glu	ata Ile	gly aaa	gag Glu 295	cat His	aga Arg	aca Thr	aaa Lys	ata Ile 300	gag Glu	gaa Glu	ctg Leu	aga Arg	912	2
car Gln 305	cat His	ctg Leu	tta Leu	arg Xaa	tgg Trp 310	gga Gly	ttt Phe	ttc Phe	aca Thr	cca Pro 315	gaa Glu	caa Gln	aaa Lys	cat His	cag Gln 320	960	)
aaa Lys	gaa Glu	cct Pro	ccm Xaa	ttc Phe 325	cak Xaa	tgg Trp	atg Met	ggt Gly	tat Tyr 330	gaa Glu	ctc Leu	cay His	cct Pro	gat Asp 335	aaa Lys	1008	}
tgg Trp	aca Thr	gta Val	cas Xaa 340	cct Pro	ata Ile	gtg Val	Leu	cca Pro 345	gaa Glu	aaa Lys	gat Asp	agc Ser	tgg Trp 350	act Thr	gtc Val	1056	i
aat Asn	Asp	ata Ile 355	cag Gln	aag Lys	tta Leu	Val	gga Gly 360	aaa Lys	ttg Leu	aat Asn	tgg Trp	gca Ala 365	agt Ser	cag Gln	att Ile	1104	:
tac Tyr																1113	
<210 <211 <212 <213	> 11 > DN	A	Immu	node	fici	ency	Vir	us (:	HIV)								

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aar tat act gca ttt acc ata cct agt ac Lys Tyr Thr Ala Phe Thr Ile Pro Ser Th 225 230	
att aga tat cag tat aat gtg ctt cca ca Ile Arg Tyr Gln Tyr Asn Val Leu Pro G 245	
gca ata ttc caa agt agc atg aca aaa at Ala Ile Phe Gln Ser Ser Met Thr Lys I 260 265	
caa aat cca gac ata gtt atc tat caa ta Gln Asn Pro Asp Ile Val Ile Tyr Gln Ty 275 280	
gga tct gac tta gaa ata gag cag cat ag Gly Ser Asp Leu Glu Ile Glu Gln His An 290 295	
aga caa cat ctg tgg aag tgg gga ttt ta Arg Gln His Leu Trp Lys Trp Gly Phe Ty 305 310	
cag aaa gaa ccc cca ttc ctt tgg atg gg Gln Lys Glu Pro Pro Phe Leu Trp Met Gl 325	
aaa tgg aca gka cag cct ata gtg ctg cc Lys Trp Thr Xaa Gln Pro Ile Val Leu Pr 340 345	
gtc aat gac ata caa aag tta gtg gga aa Val Asn Asp Ile Gln Lys Leu Val Gly Ly 355 360	
att tat cca ggg Ile Tyr Pro Gly 370	1116
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<220> <221> CDS <222> (1)(297) <223> HIV Protease	
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ggg caa cta aag gaa gct cta ata gat ac Gly Gln Leu Lys Glu Ala Leu Ile Asp Th 20 25	

tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	ata Ile	ata Ile	gly ggg	144
					gtc Val											192
					aaa Lys 70											240
cct Pro	gcc Ala	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	ctt Leu	ggt Gly	tgc Cys 95	act Thr	288
					agt Ser											336
cca Pro	gly aaa	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gag Glu	aag Lys	gag Glu	gga Gly	432
aag Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	aac Asn	agt Ser	act Thr	agg Arg	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	G1y 999	tta Leu	aaa Lys 200	aag Lys	aac Asn	aaa Lys	tca Ser	gca Ala 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggc Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gac Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acy Xaa 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gaa Glu	aca Thr	cca Pro	999 Gly 240	720
tar Xaa	ata Ile	tca Ser	gtg Val	tac Tyr 245	aat Asn	gtr Xaa	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cma Xaa	768
gca Ala	ata Ile	ttc Phe	maa Xaa 260	agt Ser	agc Ser	atg Met	aca Thr	aga Arg 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864

290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac gcn ggg Ile Tyr Ala Gly 370	1116
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<221> CDS <222> (298)(1116)	48
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<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase &lt;400&gt; 30 cct caa atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly 1</pre>	
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 30     cct caa atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly 1</pre>	96
<pre> &lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 30</pre>	96 144

tta Leu	aat Asr	ttt Phe	ccc Pro 100	o Il∈	agt Sei	cct Pro	att Ile	gaa Glu 105	ı Thr	gta Val	a cca L Pro	a gta o Val	a aaa l Lys 110	Lei	g aaa 1 Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc	c cca Pro	a aaa D Lys	gto Val	. Lys	caa Glr	ı tgo	g cca Pro	ttg Lei 125	ı Thr	gaa Glu	a gaa ı Glu	384
aaa Lys	ata Ile 130	Lys	gca Ala	tta Leu	ıgta ıVal	gaa Glu 135	: Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	Glu	aag Lys	gaa Glu	ggr Xaa	432
aaa Lys 145	att Ile	aca Thr	aaa Lys	att Ile	999 Gly 150	Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aag Lys	aaa Lys 165	Asn	agt Ser	gat Asp	aaa Lys	tgg Trp 170	Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	cca Pro	gca Ala	Gly aaa	tta Leu	aaa Lys 200	cag Gln	aaa Lys	aag Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gta Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	gta Val	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
gtt Val	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gta Val	ctc Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttt Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	agg Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 2 <b>7</b> 5	gaa Glu	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
GIY	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	gca Ala	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat (	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttc Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag a Gln 1	aaa Lys	gaa ( Glu 1	Pro .	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	Met (	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	His	cct Pro 335	gat Asp	1008
aaa t Lys :	tgg Irp	Inr v	gta ( Val ( 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu : 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056

gtc aat gac ata cag aag tta gta ggg aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 365	1104
att tat gca gga Ile Tyr Ala Gly 370	1116
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ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat gag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Glu Val Pro Ile 50 55 60	192
gaa ctc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Leu Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
ccc gtc aac ata att gga aga aat ctg wtg act caa ctt ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr 85 90 95	288
cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aga gtt ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

gy Xa	c ata a Ile	aag Lys	aaa Lys	aaa Lys 165	Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	Phe	528
ag Ar	a gaa g Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
at Il	a cca e Pro	cay His 195	ccc Pro	gca Ala	gly aaa	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctr Xaa	624
ga Asj	t gtg p Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	aga Arg	672
aag Lys 22!	g tat s Tyr 5	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
at: Ile	aga e Arg	tac Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	a ata a Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gat Asp	cct Pro	ttt Phe 270	agg Arg	aaa Lys	816
caa Glr	a aac n Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gl <sub>y</sub>	tcy Xaa 290	gac Asp	tta Leu	gaa Glu	ata Ile	gga Gly 295	cag Gln	cat His	agr Xaa	rca Xaa	aaa Lys 300	ata Ile	gaa Glu	gaa Glu	ctg Leu	912
aga Arc 305	caa Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aag Lys	aaa Lys	cat His 320	960
car Glr	aaa Lys	gaa Glu	Pro	cca Pro 325	ttt Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gtg Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aag Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gto Val	aat Asn	gac Asp 355	ant Xaa	aca Thr	gaa Glu	gtt Val	agt Ser 360	gl <sup>y</sup> aaa	aaa Lys	att Ile	gaa Glu	ttg Leu 365	ggc Gly	aag Lys	tca Ser	1104
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aag tat act gca ttt acc aya cct sgt Lys Tyr Thr Ala Phe Thr Xaa Pro Xaa 225 230		20
att aga tat cag tac aat gtg ctt cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro 245		68
gca ata ttt caa agc agc atg aca aaa Ala Ile Phe Gln Ser Ser Met Thr Lys 260 265	Ile Leu Glu Pro Phe Arg Lys	16
caa aat cca gac wta gtt wtc tat caa Gln Asn Pro Asp Xaa Val Xaa Tyr Gln 275 280		64
ggc tct gac tta gaa ata ggg cag cat Gly Ser Asp Leu Glu Ile Gly Gln His 290 295		12
aga cag cat ctg tgg aag tgg ggg ttt Arg Gln His Leu Trp Lys Trp Gly Phe 305 310	3	60
cag aaa gaa cct cca ttt ctt tgg atg Gln Lys Glu Pro Pro Phe Leu Trp Met 325		38
aaa tgg aca gta cag cct ata atg ctg Lys Trp Thr Val Gln Pro Ile Met Leu 340 345		56
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					ttg Leu											144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aaa Lys	cag Gln	tat Tyr	gag Glu 60	gag Glu	ata Ile	ccc Pro	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ttg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
					agt Ser											336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	ttw Xaa	gta Val	gaa Glu 135	att Ile	tgt Cys	gca Ala	gaa Glu	ctg Leu 140	gaa Glu	aag Lys	gaa Glu	Gly 999	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
					gac Asp											528
					agg Arg											576
ata Ile	cca Pro	cat His 195	ccc Pro	tca Ser	Gly 999	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
					acc Thr 230											720
					aat Asn											768
					agc Ser											816
					gtt Val											864

gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg ggt ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat tca ggg Ile Tyr Ser Gly 370	1116
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<220> <221> CDS <222> (1)(297) <223> HIV Protease	
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<400> 34 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1 5 10 15	48
ggg cag cta aag gaa gct cta ttr gac aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45	
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly	192
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45  gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile	192 240

4

			cct Pro					336
			aga Arg					384
			gaa Glu 135					432
			cct Pro					480
			agt Ser					528
			act Thr					576
			tta Leu					624
			ttt Phe 215					672
			ata Ile					720
			gtg Val					768
			atg Met					816
			atc Ile					864
			999 Gly 295					912
			tgg Trp					960
			cat His					1008
			ata Ile					1056

gtc aat gac ata cag aaa tta gtg ggr aaa att gaa ttt ggg cga gtc Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Ile Glu Phe Gly Arg Val 355 360 365	1104
aga ttt amc caa ggg Arg Phe Xaa Gln Gly 370	1119
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ggg caa tta aag gaa gct cta cta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 140	432
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 160	480

gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
					aga Arg											576
					gly ggg											624
					tat Tyr											672
					acc Thr 230											720
					aat Asn											768
					agc Ser											816
					gtc Val											864
					ata Ile											912
					maa Xaa 310											960
cag Gln	aaa Lys	gaa Glu	ccc Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
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					aat Asn											1104
	atg Met	cng Xaa	99													1115

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<221> CDS <222> (1) ... (297) <223> HIV Protease <221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase <400> 36 cct cag atc act ctt tgg caa cga cca gtc gtc aca ata aag gta ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Lys Val Gly 48 96 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 2.5 144 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 192 gga att gga ggt ttt rtc aaa gta aga cag tat gat caa ata ccc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 240 gaa atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr cct gyc aac ata att gga aga aat ctg ttg act cag att ggg tgc act 288 Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 90 tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 336 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg 432 Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe 480 150 gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc 528 Ala Ile Lys Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe 165 170 aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190 ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg 624 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 200 gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga 672 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 215

aag Lys 225	tat Tyr	aca Thr	gcc Ala	ttt Phe	acc Thr 230	tat Tyr	act Thr	ggt Gly	tcc Ser	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
	aga Arg															768
	ata Ile															816
	aat Asn															864
	tct Ser 290															912
	caa Gln															960
	aaa Lys															1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
	aat Asn															1104
	tac Tyr 370															1116
<21.	)> 37 L> 11 2> DN 3> Hu	.16 IA	Immu	node	fici	ency	Vir	rus (	(HIV)							
<222	)> L> CE 2> (1 3> HI	.)														
<222	l> CD 2> (2 3> Po	98).			' Rev	erse	Tra	ınscr	ipta	ıse						
cct	)> 37 cag Gln	atc														48
	caa Gln															96

tta Leu	gaa Glu	gac Asp 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	Gly 999		144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	gta Val	ccc Pro	ata Ile		192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80		240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	atg Met 90	aca Thr	cag Gln	ctt Leu	ggt Gly	tgt Cys 95	act Thr		288
					agt Ser												336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu		384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggg Gly		432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160		480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe		528
					aaa Lys												576
					gga Gly												624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	٠	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240		720
					aat Asn												768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	att Ile	tta Leu	gat Asp	cct Pro	ttt Phe 270	aga Arg	aaa Lys		816
cag Gln	aat Asn	cca Pro 275	gat Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val		864

	912
aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac gca ggg Ile Tyr Ala Gly 370	1116
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<223> HIV Protease  <221> CDS  <222> (298)(1117)  <223> Portion of HIV Reverse Transcriptase	
<221> CDS <222> (298)(1117)	48
<221> CDS <222> (298)(1117) <223> Portion of HIV Reverse Transcriptase <400> 38 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly	<b>48</b> 96
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1117) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 38 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly 1</pre>	
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1117) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 38 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly 1</pre>	96
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1117) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 38 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly 1</pre>	96 144

tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
						aaa Lys										384
						gaa Glu 135										432
						cct Pro										480
						agt Ser										528
						act Thr										576
						tta Leu										624
						ttt Phe 215										672
						ata Ile										720
						gtg Val										768
						atg Met										816
						atc Ile										864
						999 Gly 295										912
						tgg Trp										960
						ctt Leu										1008
						ata Ile										1056

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln . 355 360 365	1104											
att tan tsc agg g Ile Xaa Xaa Arg 370	1117											
<210> 39 <211> 1128 <212> DNA <213> Human Immunodeficiency Virus (HIV)												
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ggg caa cta aag gaa gct ata tta gac aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96											
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144											
gga att gga ggt ttt mtc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192											
gaa atc tgt gga cat aaa gtt atg agt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Val Met Ser Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240											
cct gtc aac ata att gga aga aat ctg atg act cag mtt ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Xaa Gly Cys Thr 85 90 95	288											
tta aat ttt ccc att agt cct att gaa act gwa cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Xaa Pro Val Lys Leu Lys 100 105 110	336											
cca ggg atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384											
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432											
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480											

		gac Asp						528
		aga Arg						576
		gly aaa						624
		tat Tyr						672
		cca Pro 230						720
		aat Asn						768
		agc Ser						816
		gtt Val						864
		ata Ile						912
		aag Lys 310						960
		ttc Phe						1008
		gcc Ala						1056
caa Gln		mag Xaa						1104
		tgc Cys						1128

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															999 Gly 240	720
	aga Arg															768
	ata Ile															816
	aat Asn															864
	tct Ser 290															912
	caa Gln															960
	aaa Lys															1008
	tgg Trp															1056
	aat Asn											att Ile	999 365	sca Xaa	agt Ser	1104
	att Ile				g											1120
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<222	)> .> CE !> (1 !> HI	)														
<222	> CD  > (2  > Po	98).				erse	Træ	nscr	ripta	ıse						
cct	> 41 caa Gln	atc														48
	caa Gln															96

						cca Pro										144
						aaa Lys 55										192
						act Thr										240
						aga Arg										288
						cct Pro										336
						aaa Lys										384
						gaa Glu 135										432
						cct Pro										480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gat Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
						act Thr										576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly ggg	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttc Phe 215	tca Ser	gtt Val	cct Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
						ata Ile										720
						gtg Val										768
						nnn Xaa										816
						nnn Xaa										864

290	tta ga Leu Gl	ı Ile G										912
aga caa cat Arg Gln His 305												960
cag aaa gaa Gln Lys Glu		Phe L										1008
aaa tgg aca Lys Trp Thr												1056
gtc Val												1059
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<222> (298) <223> Porti	_		rse Tra	anscr	ipta	.se						
	on of Hi	V Reve	aa cga	ccc	ctc	gtc						48
<223> Porti <400> 42 cct cag atc Pro Gln Ile	act ctt Thr Let 5	tgg c Trp G	aa cga ln Arg ta tta	ccc Pro	ctc Leu 10	gtc Val gga	Thr gca	Ile gat	Xaa gat	Ile 15 aca	Gly gta	<b>48</b> 96
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<223> Porti <400> 42 cct cag atc Pro Gln Ile 1 ggg caa cta Gly Gln Leu tta gaa gaa Leu Glu Glu	act ctt Thr Let 5 aag gaa Lys Gli 20 atg aat Met Asr	tgg carry G. Trp G. Ala La ttg carry Leu P. Ala La Xaa Xa	aa cga ln Arg ta tta eu Leu ca gga ro Gly 40 aa gta	ccc Pro gat Asp 25 aga Arg	ctc Leu 10 aca Thr tgg Trp	gtc Val gga Gly aaa Lys	Thr gca Ala cca Pro	Ile gat Asp aaa Lys 45 cag	yat Asp 30 atg Met	Ile 15 aca Thr ata Ile	Gly gta Val ggg Gly ata	96
<223> Porti <400> 42 cct cag atc Pro Gln Ile 1 ggg caa cta Gly Gln Leu tta gaa gaa Leu Glu Glu 35 gga att gga Gly Ile Gly	act ctt Thr Let 5 aag gaa Lys Glt 20 atg aat Met Asr ggt ttt Gly Phe	tgg c. Trp G. gct c. Ala L. ttg c. Leu P. atm a. Xaa L. aaa g.	aa cga ln Arg ta tta eu Leu ca gga ro Gly 40 aa gta ys Val 55 ct ata	ccc Pro gat Asp 25 aga Arg aga Arg	ctc Leu 10 aca Thr tgg Trp	gtc Val gga Gly aaa Lys tat Tyr	Thr gca Ala cca Pro gat Asp 60 tta	gat Asp aaa Lys 45 cag Gln	yat Asp 30 atg Met ata Ile	Ile 15 aca Thr ata Ile cyc Xaa	gta Val ggg Gly ata Ile	96 144
<223> Porti <400> 42 cct cag atc Pro Gln Ile 1 ggg caa cta Gly Gln Leu tta gaa gaa Leu Glu Glu 35 gga att gga Gly Ile Gly 50 gaa atc tgt Glu Ile Cys	act ctt Thr Let 5 aag gaa Lys Glu 20 atg aat Met Asr ggt ttt Gly Phe gga yat Gly Xaa rta att	tgg c Trp G gct c Ala L ttg c Leu P atm a Lys A 70 gga ag Gly A	aa cga ln Arg ta tta eu Leu ca gga ro Gly 40 aa gta ys ct ata la Ile ga aat	ccc Pro gat Asp 25 aga Arg aga Arg	ctc Leu 10 aca Thr tgg Trp cag Gln acr Xaa	gtc Val gga Gly aaa Lys tat Tyr gta Val 75 act	Thr gca Ala cca Pro gat Asp 60 tta Leu cag	gat Asp aaa Lys 45 cag Gln gta Val	yat Asp 30 atg Met ata Ile gga Gly	Ile 15 aca Thr ata Ile cyc Xaa ccc Pro	gta Val ggg Gly ata Ile acg Thr 80 act	96 144 192

															gaa Glu	384
		Lys													gga Gly	432
		tca Ser														480
		aag Lys														528
		ctt Leu														576
		cat His 195														624
		ggt Gly														672
		act Thr														720
att Ile	aga Arg	tay Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
		tty Phe														816
		cca Pro 275														864
		gac Asp														912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	ara Xaa 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	ccc Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
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<210> 43 <211> 1082

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ggg caa cta aag gaa gct yta ttr gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Xaa Xaa Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96											
tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144											
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192											
gaa aty tgt ggg cat aaa gct ata ggt aca gta tta gta ggg cct aca Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240											
cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288											
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336											
cca gga atg gat ggc ccc aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384											
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432											
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480											
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528											
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576											
ata ccg cat ccc gca ggg tta aaa aag aaa aag tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624											

gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aaa Lys 225	tat Tyr	ast Xaa	gca Ala	ttt Phe	acc Thr 230	ata Ile	ccg Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
			cag Gln													768
			caa Gln 260													816
			gac Asp													864
			ttg Leu													912
			ctg Leu													960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	330 Gly 399	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	caa Gln	ccg Pro	ata Ile	gag Glu	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gaa Glu	agc Ser 350	tgg Trp	act Thr	1056
			ata Ile					gg								1082
<211 <212	)> 44 .> 11 !> DN !> Hu	16 IA	Immu	ınode	fici	ency	· Vir	rus (	(HIV)							
<222	> CI > (1	)	(297 otea				ı									
<222		98).	(1 on of			erse	Tra	ınscr	ipta	ıse						
cct		atc	act Thr													48
Gly 999			aag Lys 20													96

tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	tta Leu	cca Pro	gga Gly 40	aaa Lys	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	ata Ile	ata Ile	G1y 999	1	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	gcc Ala	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	ccc Pro	ata Ile	1	192
gaa Glu 65	atc Ile	tka Xaa	gga Gly	cat His	aaa Lys 70	gtt Val	ata Ile	ggt Gly	aca Thr	gtc Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	2	240
cct Pro	gcc Ala	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	2	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	3	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	3	384
	ata Ile 130															4	132
aaa Lys 145	att Ile	tca Ser	aag Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	4	180
	ata Ile															5	528
	gaa Glu															5	576
ata Ile	cca Pro	cat His 195	ccc Pro	tca Ser	Gly 333	tta Leu	aaa Lys 200	aag Lys	aam Xaa	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	6	524
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	$\epsilon$	572
	tat Tyr															7	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	7	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aga Arg 265	atc Ile	cta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	8	316
cag Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	çaa Gln	tac Tyr	gtg Val	gat Asp	gac Asp 285	ttg Leu	ctt Leu	gta Val	ε	364

	912
aga caa cat ctg ttg agg tgg ggg ttt atc aca cca gac gaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Ile Thr Pro Asp Glu Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gay agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
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<220> <221> CDS <222> (1)(297) <223> HIV Protease	
<221> CDS <222> (298)(1116) <223> Portion of HIV Reverse Transcriptase	
<222> (298)(1116)	48
<222> (298)(1116) <223> Portion of HIV Reverse Transcriptase <400> 45 cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly	<b>48</b> 96
<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 45 cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly 1</pre>	
<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 45 cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly 1</pre>	96
<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 45 cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly 1</pre>	96 144

	ccc Pro 100						aag Lys	336
	gat Asp							384
	gca Ala							432
	aaa Lys							480
	aaa Lys							528
	aat Asn 180							576
	ccc Pro							624
	gat Asp							672
	gca Ala							720
	caa Gln							768
	caa Gln 260							816
	gaa Glu							864
	tta Leu							912
	ctg Leu							960
	ccc Pro							1008
	ata Ile 340							1056

gtc aat gac cta cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Leu Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116
<210> 46 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
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<pre>&lt;400&gt; 46 cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly 1 5 10 15</pre>	48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gag att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 160	480
-77 -	

										Arg		tta Leu				528
												gtt Val			gga Gly	576
												gta Val 205				624
												gaa Glu				672
aaa Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
												aaa Lys				768
gca Ala	ata Ile	ttc Phe	caa Gln 260	tgt Cys	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
												gat Asp 285				864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gga Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	acc Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttt Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gtr Xaa 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
	tac Tyr 370															1116

<220>

<sup>&</sup>lt;210> 47 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298) ... (1116) <223> Portion of HIV Reverse Transcriptase <400> 47 48 cct caa atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 96 144 tta gaa gac atg tgt ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 192 gga att gga ggt ttt atc aaa gta aga caa tat gat cag gta gcc atg Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ala Met gaa atc tgt gga cat aag gct ata ggt aca gta tta ata gga cct aca 240 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 288 ect gtc aac ata att gga aga aat etg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 90 tta aat ttt ccc att agc cct att gaa act gta ccm gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Xaa Val Lys Leu Lys cca ggr atg gat ggt cca agg gtt aaa caa tgg cca ttg aca gaa gaa 384 Pro Xaa Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu aaa ata ara gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432 Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 480 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt 528 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe aga gaa ctt aat aag aaa act caa gac tty tgg gaa gtt caa tta ggr 576 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa 180 ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctt 624 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 200 672 gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gat ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220

aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
			caa Gln													768
			caa Gln 260													816
			gac Asp													864
			tta Leu													912
			ctg Leu													960
			ссу Хаа													1008
			gta Val 340													1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aar Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
_	tat Tyr 370															1116
<211 <212	)> 48 .> 11 !> DN !> Hu	.15 IA	Immu	ınode	fici	ency	. Vir	rus (	HIV)							
<222	> CE !> (1	.)	(297 otea													
<222		98).	(1 on of	-	' Rev	erse	Tra	ınscr	ipta	ıse						
cct		atc	act Thr													48
			aag Lys 20													96

ata Ile	gaa Glu	gac Asp 35	ata Ile	gaa Glu	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	Gly 999	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aaa Lys	cag Gln	tat Tyr	gag Glu 60	cag Gln	gta Val	ccc Pro	ata Ile	192
gaa Glu 65	ctc Leu	tgt Cys	gjå aaa	cgt Arg	aaa Lys 70	act Thr	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aac Asn	ctg Leu	atg Met 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
					cca Pro											384
					ata Ile											432
					999 Gly 150											480
					gac Asp											528
					aaa Lys											576
ata Ile	cca Pro	cat His 195	cct Pro	gca Ala	gly aaa	tta Leu	aaa Lys 200	aag Lys	aag Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ttg Leu	624
					tat Tyr											672
					acc Thr 230											720
					aat Asn											768
					agc Ser											816
					gtt Val											864

290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tcc car ga Ile Ser Gln 370	1115
<210> 49 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (1)(297) <223> HIV Protease	
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<222> (298)(1116)	48
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<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 49 cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly 1</pre>	
<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 49 cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly 1</pre>	96
<pre>&lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 49 cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly 1</pre>	96 144

tta aat tt Leu Asn Ph	ccc att Pro Ile	agt cct Ser Pro	Ile G	aa act lu Thr	gta cc Val Pr	a gta o Val	aag Lys 110	tta Leu	aag Lys	336
cca gga at Pro Gly Me 11	. Asp Gly	cca aaa Pro Lys	gtt a Val L 120	aa caa ys Gln	tgg cc Trp Pr	a ttg to Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa ata aa Lys Ile Ly 130	a gca tta s Ala Leu	gta gaa Val Glu 135	atc to	gt aca ys Thr	gaa at Glu Me 14	t Glu	aag Lys	gaa Glu	Gly ggg	432
aaa att tc Lys Ile Se 145	a aaa att r Lys Ile	ggg cct Gly Pro 150	gaa a Glu A	at cca sn Pro	tac aa Tyr As 155	it act in Thr	cca Pro	gta Val	ttt Phe 160	480
gcc ata aa Ala Ile Ly	g aaa aag s Lys Lys 165	gac agt Asp Ser	act a Thr L	aa tgg ys Trp 170	aga aa Arg Ly	a tta s Leu	gta Val	gat Asp 175	ttc Phe	528
aga gaa ct Arg Glu Le	aat aag Asn Lys 180	aaa act Lys Thr	Gln A	ac ttc sp Phe .85	tgg ga Trp Gl	a gtt u Val	caa Gln 190	tta Leu	gga Gly	576
ata cca ca Ile Pro Hi 19	s Pro Ala	ggg tta Gly Leu	aaa a Lys L 200	ag aam ys Xaa	aaa to Lys Se	a gta r Val 205	aca Thr	gta Val	ctg Leu	624
gat gtg gg Asp Val Gl 210	gat gca Asp Ala	tat ttt Tyr Phe 215	tca g Ser V	tt ccc al Pro	tta ga Leu As 22	p Lys	gaa Glu	ttc Phe	agg Arg	672
aag tat ac Lys Tyr Th 225	gca ttt Ala Phe	cca tcc Pro Ser 230	cta g Leu V	tt ata al Ile	aac aa Asn As 235	it gag in Glu	aca Thr	cca Pro	gga Gly 240	720
atc aga ta Ile Arg Ty:	cag tac r Gln Tyr 245	aat gtg Asn Val	ctt c Leu P	ca cag ro Gln 250	gga tg Gly Tr	g aaa p Lys	gga Gly	tca Ser 255	cca Pro	768
gca ata tt Ala Ile Ph	caa agt Gln Ser 260	agc atg Ser Met	Thr L	aa atc ys Ile 65	tta ga Leu Gl	ng cct .u Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa aat cc Gln Asn Pro 27	o Asp Ile	gtt atc Val Ile	tat c Tyr G 280	aa tac In Tyr	gtg ga Val As	at gat sp Asp 285	ttg Leu	tat Tyr	gta Val	864
gga tct ga Gly Ser As 290	c tta gaa p Leu Glu	ata ggg Ile Gly 295	cag c Gln H	at aga lis Arg	aca aa Thr Ly 30	rs Val	gag Glu	gag Glu	ctg Leu	912
aga caa ca Arg Gln Hi 305	t ctg ttg s Leu Leu	agg tgg Arg Trp 310	gga t Gly P	tt acc he Thr	aca co Thr Pr 315	a gac o Asp	aaa Lys	aaa Lys	cat His 320	960
cag aaa ga Gln Lys Gl	g cct cca ı Pro Pro 325	Phe Leu	tgg a Trp M	tg ggt Met Gly 330	tat ga Tyr Gl	a ctc u Leu	cat His	cct Pro 335	gat Asp	1008
aaa tgg ac Lys Trp Th	a gta cag r Val Gln 340	cct ata Pro Ile	Val L	tg cca eu Pro 45	gaa aa Glu Ly	a gac vs Asp	agc Ser 350	tgg Trp	act Thr	1056

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
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<220> <221> CDS <222> (1)(297) <223> HIV Protease	
<221> CDS <222> (298)(1116) <223> Portion of HIV Reverse Transcriptase	
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gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttk gtc aaa gta aga cag tat gat cag ata cct gta Gly Ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	192
gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca Glu Ile Cys Gly His Lys Xaa Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 . 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 160	480

			aaa Lys													528
			aat Asn 180													576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly aaa	tta Leu	mam Xaa 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gtg Val	cta Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	tat Tyr 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
			gca Ala													720
			cag Gln													768
			cag Gln 260													816
			gaa Glu													864
			tta Leu													912
			ctg Leu													960
			cct Pro		_			_							_	1008
		-	gta Val 340					_		_		_	_			1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aaa Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
	tat Tyr 370															1116

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<sup>&</sup>lt;210> 51 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase <400> 51 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 48 96 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 144 gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata 192 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca 240 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288 Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr 90 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt 480 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 155 gcc ata aag aaa aaa aac agt act aaa tgg aga aaa tta gta gat ttc 528 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg 624 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg 672 Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg 210 215 220

aag tat Lys Ty: 225	act Thr	gca Ala	ttc Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
gtt aga Val Arg															768
gca ata Ala Ile															816
caa aat Gln Asr															864
gga tct Gly Ser 290	Asp														912
aga caa Arg Glr 305															960
cag aaa Gln Lys	gaa Glu	ccc Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa tgg Lys Trp															1056
gtc aat Val Asn	gac Asp 355	ata Ile	cag Gln	aaa Lys	tta Leu	gtg Val 360	G1y 999	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att tat Ile Tyr 370	Āla														1116
<210> 5 <211> 1 <212> D <213> H	116 NA	Immu	ınode	efici	.ency	. Vir	cus (	(HIV)							
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ggg caa Gly Gln															96

															ggg Gly	144
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						gct Ala										240
						aga Arg										288
						cct Pro										336
						aaa Lys										384
						gaa Glu 135										432
						ccc Pro										480
						agt Ser										528
						act Thr										576
						tta Leu										624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	atr Xaa	aac Asn 235	aat Asn	gaģ Glu	aaa Lys	cca Pro	999 Gly 240	720
						gtg Val										768
						atg Met										816
car Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864

	912
aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960
cag aaa gaa ccg cca ttc ctt tgg atg ggt tat gaa cta cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg acg gta cag cct ata aag ctg cca gaa aaa gat agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tay gca ggg Ile Tyr Ala Gly 370	1116
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<221> CDS <222> (298)(1116)	48
<221> CDS <222> (298)(1116) <223> Portion of HIV Reverse Transcriptase <400> 53 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	48 96
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase &lt;400&gt; 53 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 53 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	96
<pre>&lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase &lt;400&gt; 53 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	96 144



tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gag Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	Gly 999	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
													caa Gln 190			576
atc Ile	cca Pro	cat His 195	cct Pro	gca Ala	ggg ggg	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	cgg Arg	672
_			_					_					aca Thr			720
													gga Gly			768
													ttt Phe 270			816
													ttg Leu			864
gga Gly	tct Ser 290	gac Asp	cta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	gca Ala	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
													aaa Lys			960
_		_						_					cat His		-	1008
													agc Ser 350			1056

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca gga Ile Tyr Ala Gly 370	1116
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ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr 65 70 75 80	240
cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 160	480

gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	gta Val	gta Val	gat Asp 175	ttc Phe	528
								gac Asp 185								576
								aag Lys								624
								gtt Val								672
								agt Ser								720
								cca Pro								768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
								caa Gln								864
								cac His								912
								ttt Phe								960
								atg Met								1008
								ctg Leu 345								1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	Gly 999	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
		gca Ala	Gly ggg													1116

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<sup>&</sup>lt;210> 55 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298) ... (1116) <223> Portion of HIV Reverse Transcriptase cct caa atc act ctt tgg caa cga ccc ctc gtc gca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly 48 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gtc Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 96 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 144 gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta 192 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val 240 gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr 288 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 90 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg 432 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc 528 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe aga gaa ctt aat aag aaa acg caa gac ttc tgg gaa gtt caa tta gga 576 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 190 180 185 624 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 200 672 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220

aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	gta Val	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
			cag Gln													768
			caa Gln 260													816
			gac Asp													864
			tta Leu													912
			ctg Leu	_		~ ~						_		_		960
			cct Pro													1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	ktg Xaa	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
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<222	> CI > (1	.)	(297 otea													
<222		98).	(1 on of		Rev	erse	Tra	ınscr	ipta	se						
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gly ggg	caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96

tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aaa Lys	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	gly aaa	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	acc Thr	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100 <sub>,</sub>	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
					gta Val											432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
					gat Asp											528
					aga Arg											576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly aaa	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	cta Leu	624
					tat Tyr											672
					acc Thr 230											720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
					agc Ser											816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864

290	raa ata Xaa Ile	gag cag Glu Gln 295	cat aga His Arg	aca aaa Thr Lys 300	ata gag Ile Glu	gaa ctg Glu Leu	912
aga caa cat ctg Arg Gln His Leu 305	ttg agg Leu Arg 310	tgg gga Trp Gly	ttt acc Phe Thr	aca cca Thr Pro 315	gac aaa Asp Lys	aag cat Lys His 320	
cag aaa gaa cct Gln Lys Glu Pro	cca ttc Pro Phe 325	ctt tgg Leu Trp	atg ggt Met Gly 330	tat gaa Tyr Glu	ctc cat Leu His	cct gat Pro Asp 335	1008
aaa tgg aca gta Lys Trp Thr Val 340						Trp Thr	
gtc aat gac ata Val Asn Asp Ile 355	cag aag Gln Lys	tta gtg Leu Val 360	gga aaa Gly Lys	tta aat Leu Asn	tgg gca Trp Ala 365	agt cag Ser Gln	1104
att tat cca ggg Ile Tyr Pro Gly 370							1116
<210> 57 <211> 1116 <212> DNA <213> Human Imm	unodefic	iency Vi	rus (HIV)	)			
<220> <221> CDS <222> (1)(29' <223> HIV Protes	-						
(223) HIV FIOLE							
<pre>&lt;221&gt; CDS &lt;222&gt; (298)() &lt;223&gt; Portion of</pre>		verse Tra	anscripta	ase			
<221> CDS <222> (298)(	f HIV Rev	caa cga	ccc ctc	gtc aca	gta aag Val Lys	tta ggg Leu Gly 15	48
<221> CDS <222> (298)( <223> Portion of <400> 57 cct cag atc act Pro Gln Ile Thr	ctt tgg Leu Trp 5 gaa gtt	caa cga Gln Arg	ccc ctc Pro Leu 10 gat aca	gtc aca Val Thr gga gca	Val Lys gat gat	Leu Gly 15 aca gta	<b>48</b> 96
<221> CDS <222> (298)(3 <223> Portion of <400> 57 cct cag atc act Pro Gln Ile Thr 1 ggg caa cta atg Gly Gln Leu Met	ctt tgg Leu Trp 5 gaa gtt Glu Val	caa cga Gln Arg cta tta Leu Leu cca gga	ccc ctc Pro Leu 10 gat aca Asp Thr 25	gtc aca Val Thr gga gca Gly Ala	Val Lys gat gat Asp Asp 30 aaa atg	Leu Gly 15 aca gta Thr Val ata ggg	
<221> CDS <222> (298)(3 <223> Portion of <400> 57 cct cag atc act Pro Gln Ile Thr 1 ggg caa cta atg Gly Gln Leu Met 20 rta gaa gaa ata Xaa Glu Glu Ile	ctt tgg Leu Trp 5 gaa gtt Glu Val agt tta Ser Leu	caa cga Gln Arg cta tta Leu Leu cca gga Pro Gly 40 aaa gta	ccc ctc Pro Leu 10 gat aca Asp Thr 25 aga tgg Arg Trp	gtc aca Val Thr gga gca Gly Ala aaa cca Lys Pro	Val Lys gat gat Asp Asp 30 aaa atg Lys Met 45 cag gta	Leu Gly 15  aca gta Thr Val  ata ggg Ile Gly  ccc tta	96
<221> CDS <222> (298)(3) <223> Portion of <400> 57 cct cag atc act Pro Gln Ile Thr 1 ggg caa cta atg Gly Gln Leu Met 20 rta gaa gaa ata Xaa Glu Glu Ile 35 gga att gga ggt Gly Ile Gly Gly	ctt tgg Leu Trp 5 gaa gtt Glu Val agt tta Ser Leu ttt gtc Phe Val aaa aag	caa cga Gln Arg  cta tta Leu Leu  cca gga Pro Gly 40  aaa gta Lys Val 55	ccc ctc Pro Leu 10 gat aca Asp Thr 25 aga tgg Arg Trp aaa cag Lys Gln	gtc aca Val Thr  gga gca Gly Ala  aaa cca Lys Pro  tat gat Tyr Asp 60 gta tta	yal Lys gat gat Asp Asp 30 aaa atg Lys Met 45 cag gta Gln Val	aca gta Thr Val  ata ggg Ile Gly  ccc tta Pro Leu  cct aca	96

tta Leu	aat Asn	ttc Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
						gaa Glu 135										432
						cct Pro										480
						agt Ser										528
						acs Xaa										576
						tta Leu										624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	cca Pro	gac Asp	ttc Phe	agg Arg	672
						ata Ile										720
						gtg Val										768
						atg Met										816
						atc Ile										864
						gag Glu 295										912
						tgg Trp										960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
						ata Ile										1056

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
<210> 58 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (1)(297) <223> HIV Protease	
<221> CDS <222> (298)(1116) <223> Portion of HIV Reverse Transcriptase	
<pre>&lt;400&gt; 58 cct caa atc act ctt tgg caa cga ccc cta gtt aca ata aaa ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1 5 10 15</pre>	48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ctc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

			aaa Lys													528
		-1-	-1-	165				-1 -	170					175		
			aat Asn 180													576
			cca Pro													624
			gat Asp													672
			gca Ala													720
			cag Gln													768
			caa Gln 260													816
			gac Asp													864
			tta Leu													912
aga Arg 305	cag Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cca Pro 335	gat Asp	1008
			gta Val 340													1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
		gca Ala														1116

<210> 59 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase cct caa atc act ctt tgg caa cga ccc tta gtc aca ata aag ata grg 48 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Xaa ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta 96 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly 144 gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata 192 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile 240 gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 288 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 336 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 384 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 432 aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 528 gcm ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 576 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta 624 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 672 gat gtq ggt gat gca tat ttc tca gtt ccc tta gac caa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg 215 220

			gca Ala													720
			cag Gln													768
			caa Gln 260													816
			gaa Glu													864
			tta Leu													912
			ctg Leu													960
			cct Pro													1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	act Thr	ata Ile	gaa Glu	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gat Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
	tac Tyr 370															1116
<211 <212	<210> 60 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)															
<221 <222	<220> <221> CDS <222> (1)(297) <223> HIV Protease															
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cct	> 60 caa Gln	atc	act Thr	ctt Leu 5	tgg Trp	cag Gln	cga Arg	ccc Pro	cty Xaa 10	gtc Val	aca Thr	ata Ile	aag Lys	ata Ile 15	Gly aaa	48
			aaa Lys 20													96

															ggg Gly	14	4
												cag Gln			rta Xaa	19	2
												ata Ile				24	0
												ctt Leu				. 28	8
												gta Val				336	6
												ttg Leu 125				384	4
												gaa Glu				432	2
												act Thr				480	)
												tta Leu				528	3
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aar Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576	5
												gta Val 205				624	ī
												aaa Lys				672	2
												gag Glu				720	)
												aaa Lys				768	3
												cct Pro				816	5
caa Gln	aat Asn	cca Pro 275	cac His	ata Ile	gtt Val	att Ile	ttt Phe 280	caa Gln	tat Tyr	gtg Val	gat Asp	gac Asp 285	ttg Leu	tat Tyr	gta Val	864	Ė

gca tct gac tta gaa ata gag cag cat aga aca aa Ala Ser Asp Leu Glu Ile Glu Gln His Arg Thr Ly 290 295 30	s Ile Glu Glu Leu											
aga caa cat ttg ttg agg tgg gga ctc acc aca cc Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pr 305 310 315	a gac aaa aaa cat 960 o Asp Lys Lys His 320											
caa aaa gaa cct cca ttc ctt tgg atg ggt tat ga Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Gl 325 330												
aaa tgg aca gta cag ccc ata acg ctg cca gaa aa Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Ly 340 345												
gtc aat gac ata cag aag tta gtg gga aaa ttg aa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu As: 355 360												
att tat gca ggg Ile Tyr Ala Gly 370	1116											
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1 5 10	15											
ggg gca agt aaa gaa gct cta tta gat aca gga gca Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala 20 25	15 a gat gat aca gta 96											
ggg gca agt aaa gaa gct cta tta gat aca gga gca Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala	15 a gat gat aca gta 96 a Asp Asp Thr Val 30 a aaa atg ata ggg 144											
ggg gca agt aaa gaa gct cta tta gat aca gga gca Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala 20 25  tta gaa gaa ata aat ttg cca ggg rag tgg aaa cca Leu Glu Glu Ile Asn Leu Pro Gly Xaa Trp Lys Pro	a gat gat aca gta 96 Asp Asp Thr Val 30  a aaa atg ata ggg 144 Lys Met Ile Gly 45  c cag ata ccc gta 192 Gln Ile Pro Val											
ggg gca agt aaa gaa gct cta tta gat aca gga gca Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala 20 25  tta gaa gaa ata aat ttg cca ggg rag tgg aaa cca Leu Glu Glu Ile Asn Leu Pro Gly Xaa Trp Lys Pro 35 40  gga att gga ggt ttt atc aaa gta aga cag tmt gat Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Xaa Asp	a gat gat aca gta 96 Asp Asp Thr Val 30  a aaa atg ata ggg 144 D Lys Met Ile Gly 45  c cag ata ccc gta 192 Gln Ile Pro Val											

tta aa Leu As	t ttt n Phe	ccc Pro 100	atc Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca gg Pro Gl	a atg y Met 115	Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	tta Leu 125	aca Thr	gag Glu	gaa Glu	384
aaa at Lys Il 13	e Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	Gly 999	432
aaa at Lys Il 145	t tca e Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	ata Ile	ttt Phe 160	480
gcc at Ala Il	a aag e Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga ga Arg Gl	a ctt u Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	cag Gln 190	tta Leu	gga Gly	576
ata cc Ile Pr	a cat o His 195	Pro	gca Ala	gly ggg	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat gt Asp Va 21	l Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	agc Ser	ttc Phe	agg Arg	672
aag ta Lys Ty 225															720
rca ag Xaa Ar	a tat g Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca at Ala Il															816
caa aa Gln As		Ğlu													864
gga to Gly Se 29	r Asp	tta Leu	gag Glu	ata Ile	gag Glu 295	caa Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga ca Arg Gl 305															960
cag aa Gln Ly															1008
aaa tg Lys Tr	g aca p Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aag Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104												
att tat cca ggg Ile Tyr Pro Gly 370	1116												
<210> 62 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)													
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96												
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144												
gga att gga ggt ttt atc aaa gta aga caa tat gat cag ata gcc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile 50 55 60	192												
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240												
cct gtc aac ata att gga aga aat ctg atg act cag att ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288												
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys 100 105 110	336												
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384												
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432												
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480												

gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	aat Asn	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly ggg	cta Leu	aaa Lys 200	aag Lys	aay Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtc Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tac Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
rtt Xaa	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
tca Ser	ata Ile	ttc Phe	caa Gln 260	tgt Cys	agc Ser	atg Met	acg Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
cag Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	trt Xaa 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gca Ala	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gag Glu 295	cag Gln	cat His	aga Arg	ata Ile	aaa Lys 300	ata Ile	gag Glu	gaa Glu	cta Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	yat Xaa 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gar Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	. 1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	ttr Xaa	gtg Val 360	gga Gly	aaa Lys	ctg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
	tac Tyr 370															1116
<210> 63 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)																
<22								<del>-</del>	<b>-</b> * 1							

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase <400> 63 cct caa atc act ctt tgg caa cga ccc gtt gtt aca gta agg ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Val Arg Ile Gly 48 gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val 96 144 tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta 192 Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr 288 90 tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu 115 aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga 432 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly aaa att tca aga ata ggg cct gaa aat cca tac aat act cca ata ttt 480 Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 150 gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc 528 Ala Ile Lys Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg 624 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu gat gtg ggt gat gca tat ttt tca qtt ccc tta cat qaa qac ttt aqa 672 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg 210 215

aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 235 235 240	720											
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca ccg Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768											
gca ata ttc caa agt agc atg acc aaa atc tta gaa cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816											
caa aat cca gaa atg gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864											
gga tct gac tta gaa ata ggg cag cat aga ata aaa ata gag gaa tta Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu 290 295 300	912											
agg gaa cac cta ttg aag tgg gga ttt ttc acc cca gac gaa aag cat Arg Glu His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His 305 310 315 320	960											
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctt cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008											
aaa tgg aca gtg cag cct ata aaa ctg cca gaa aaa gaa agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056											
gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104											
att tat cca gga Ile Tyr Pro Gly 370	1116											
<210> 64 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)												
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<400> 64 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1 5 10 15	48											
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96											

												aaa Lys 45				144
gga Gly	att Ile 50	gga Gly	ggy Xaa	ttt Phe	rtc Xaa	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	syc Xaa	ata Ile	192
												gta Val				240
												ctt Leu				288
												gta Val				336
												tta Leu 125				384
												gaa Glu				432
												act Thr				480
gct Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	gct Ala	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
agg Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gly aaa	576
												gta Val 205				624
												caa Gln				672
												gag Glu				720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gar Glu	ata Ile	rtt Xaa	Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864

gga tct gac ttr gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Xaa Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca gga Ile Tyr Ala Gly 370	1116
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<pre>&lt;400&gt; 65 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly</pre>	48
1 5 10 11e thi field trip Grif Arg Fro Tre Var Till Tre Bys Tre Gry	
	96
1 5 10 15  ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30  tta gaa gac atc aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	96
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20  tta gaa gac atc aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 40  gga att gga ggt ttt gtc aaa gta aga gag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Glu Tyr Asp Gln Val Pro Ile	96 144

tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	3	36
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	3	84
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gar Glu 135	atc Ile	tgt Cys	aca Thr	gaa Glu	ttg Leu 140	gaa Glu	aag Lys	gaa Glu	gga Gly	4	32
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aay Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	4	80
gct Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	5	28
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	5	76
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	Gly ggg	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctr Xaa	6	24
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	6	72
aag Lys 225	tac Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	7	20
rtt Xaa	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	7	68
						atg Met										8	16
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	att Ile	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	8	64
gga Gly	tct Ser 290	gat Asp	ttg Leu	gaa Glu	ata Ile	gag Glu 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	cta Leu	9	12
aga Arg 305	gaa Glu	cat His	ctg Leu	tgg Trp	aag Lys 310	tgg Trp	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	9	60
cag Gln	aag Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	10	80
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	aag Lys	ytg Xaa 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	10	56

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Xaa Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

						agt Ser									ttc Phe	528
						act Thr										576
						tta Leu										624
						ttt Phe 215										672
aar Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	wac Xaa 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	krc Xaa 245	aat Asn	gtg Val	yyt Xaa	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tcm Xaa 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	mam Xaa 260	agt Ser	agc Ser	ayg Xaa	aca Thr	aaa Lys 265	att Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ttg Leu	912
agg Arg 305	caa Gln	cat His	ttg Leu	ttg Leu	agg Arg 310	tgg Trp	ggr Xaa	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	ara Xaa	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gag Glu	cct Pro	cca Pro 3 <b>2</b> 5	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	aaa Lys	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gay Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
	tat Tyr 370	gca Ala	gly aaa													1116
<210 <211																

<220>

<sup>&</sup>lt;211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298) ... (1119) <223> Portion of HIV Reverse Transcriptase <400> 67 cct caa atc act ctt tgg caa cga cca ata gtc aca ata aag ata ggg 48 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 96 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 144 cta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata tcc ata 192 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile gaa atc tgt ggg cat aaa gtt aca ggt aca gtg tta ata gga cct aca 240 Glu Ile Cys Gly His Lys Val Thr Gly Thr Val Leu Ile Gly Pro Thr cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 90 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu aaa ata aaa gca ttg gta gaa att tgt gca gaa atg gaa aag gaa ggg 432 Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Met Glu Lys Glu Gly caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt 480 Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe gtc ata aag aaa aaa gac ggt act aac tgg aga aaa tta ata gat ytc 528 Val Ile Lys Lys Lys Asp Gly Thr Asn Trp Arg Lys Leu Ile Asp Xaa aga gaa ctt aat aag aga act caa gat ttc tgg gaa att caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg 624 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg 672 Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg 210 215 220

															999 Gly 240	720
			cag Gln												cca Pro	768
			caa Gln 260													816
			gac Asp													864
gca Ala	tct Ser 290	gat Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
			cta Leu													960
			cct Pro													1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
			gly aaa													1119
<211 <212	> 68 .> 11 !> DN !> Hu	.19 IA	Immu	node	fici	ency	Vir	rus (	HIV)							
<222	> CI > (1	.)	(297 otea													
	> (2	98).	(1 on of			erse	Tra	ınscr	ipta	ıse						
<400 cct Pro 1	caa	atc	act Thr	ctt Leu 5	tgg Trp	caa Gln	cga Arg	ccc Pro	ctc Leu 10	gtc Val	aca Thr	ata Ile	aag Lys	ata Ile 15	gly aaa	48
gga Gly	caa Gln	cta Leu	aaa Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96

															Gly aaa	144
					atc Ile										ata Ile	192
					aaa Lys 70										aca Thr 80	240
					gga Gly											288
					agt Ser											336
					cca Pro											384
					gta Val											432
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					gac Asp											528
					aga Arg											576
					gly aaa											624
					tat Tyr											672
					acc Thr 230											720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
					agc Ser											816
					rtt Xaa											864

290	gaa ata gga Glu Ile Gly 295	Gln His Arg	aca aaa ata gaa Thr Lys Ile Glu 300	gaa ctg 912 Glu Leu
aga caa cat ctg Arg Gln His Leu 305				
cag aaa gaa cct Gln Lys Glu Pro				
aaa tgg aca gta Lys Trp Thr Val 340				
gtc aat gac ata Val Asn Asp Ile 355				
att tat cca ggg Ile Tyr Pro Gly 370		-		1119
<210> 69 <211> 1119 <212> DNA <213> Human Immu	nodeficiency	y Virus (HIV)		
<220> <221> CDS <222> (1)(297 <223> HIV Protea				
<221> CDS <222> (298)(1 <223> Portion of		e Transcripta	se	
<222> (298)(1	HIV Reverse	cga ccc cty	gtc aca ata aag	ata ggg 48 Ile Gly 15
<222> (298)(1 <223> Portion of <400> 69 cct cag atc act Pro Gln Ile Thr	HIV Reverse ctt tgg caa Leu Trp Gln 5 gaa gct mta	cga ccc cty Arg Pro Xaa 10	gtc aca ata aag Val Thr Ile Lys gga gca gat gat	Ile Gly 15 aca gtg 96
<222> (298)(1 <223> Portion of <400> 69 cct cag atc act of Pro Gln Ile Thr 1 1 ggg caa yta aag Gly Gln Xaa Lys of	HIV Reverse ctt tgg caa Leu Trp Gln 5 gaa gct mta Glu Ala Xaa aat ttg cca	cga ccc cty Arg Pro Xaa 10  tta gay aca 1 Leu Asp Thr 25  gga aga tgg	gtc aca ata aag Val Thr Ile Lys gga gca gat gat Gly Ala Asp Asp 30 aaa cca aaa ata	Ile Gly 15  aca gtg 96 Thr Val  ata ggg 144
<pre>&lt;222&gt; (298)(1 &lt;223&gt; Portion of &lt;400&gt; 69 cct cag atc act of Pro Gln Ile Thr 1  ggg caa yta aag g Gly Gln Xaa Lys of 20  tta gaa gaa atg a Leu Glu Glu Met 2</pre>	HIV Reverse  ctt tgg caa  Leu Trp Gln  5  gaa gct mta Glu Ala Xaa  aat ttg cca Asn Leu Pro  ttt atc aaa	cga ccc cty and arg Pro Xaa 10  tta gay aca 1 Leu Asp Thr 25  gga aga tgg Gly Arg Trp 40  gta aga gag	gtc aca ata aag Val Thr Ile Lys gga gca gat gat Gly Ala Asp Asp 30 aaa cca aaa ata Lys Pro Lys Ile 45 tat gag cag ata	Ile Gly 15  aca gtg 96 Thr Val  ata ggg 144 Ile Gly  caa gta 192
<pre>&lt;222&gt; (298)(1 &lt;223&gt; Portion of &lt;400&gt; 69 cct cag atc act Pro Gln Ile Thr 1  ggg caa yta aag Gly Gln Xaa Lys 20  tta gaa gaa atg 2 Leu Glu Glu Met 2 35  gga att gga ggt Gly Ile Gly Gly ;</pre>	HIV Reverse  ctt tgg caa Leu Trp Gln 5  gaa gct mta Glu Ala Xaa  aat ttg cca Asn Leu Pro  ttt atc aaa Phe Ile Lys 55  cat aag gct	cga ccc cty Arg Pro Xaa 10  tta gay aca Leu Asp Thr 25  gga aga tgg Gly Arg Trp 40  gta aga gag Val Arg Glu 4	gtc aca ata aag Val Thr Ile Lys  gga gca gat gat Gly Ala Asp Asp 30  aaa cca aaa ata Lys Pro Lys Ile 45  tat gag cag ata Tyr Glu Gln Ile 60  gta tta ata gga	Ile Gly 15  aca gtg 96 Thr Val  ata ggg 144 Ile Gly  caa gta 192 Gln Val  cct aca 240

									Thr					Leu	aag Lys	336
			Āsp					Lys					Thr		gaa Glu	384
aaa Lys	ata Ile 130	Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	ttg Leu 140	gaa Glu	aag Lys	gaa Glu	gga Gly	432
	Ile											acy Xaa				480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	ccg Pro	cat His 195	ccc Pro	gca Ala	Gly aaa	tta Leu	aag Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctr Xaa	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tac Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	gga Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gaa Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	car Gln	tac Tyr	atg Met	gat Asp	gac Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	cta Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	tkg Xaa	agg Arg 310	tgg Trp	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctr Xaa 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat tca ggg att Ile Tyr Ser Gly Ile 370	1119
<210> 70 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (1)(297) <223> HIV Protease	
<221> CDS <222> (298)(1119) <223> Portion of HIV Reverse Transcriptase	
<pre>&lt;400&gt; 70 cct caa atc act ctt tgg caa cga ccc cty gtc kca ata aag gta ggr Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Xaa Ile Lys Val Xaa 1 5 10 15</pre>	48
ggg caa mta aag gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gat cag gta arc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aay ctg ttg aca cag att ggt tgy act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca ara gty aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Xaa Xaa Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aar gca tta atg gaa att tgt gca gay atg gaa aag gaa ggr Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Asp Met Glu Lys Glu Xaa 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

													gta Val			528
													caa Gln 190			576
ata Ile	cca Pro	cat His 195	ccy Xaa	gca Ala	Gly 999	tta Leu	aaa Lys 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ttg Leu	624
													gac Asp			672
													aca Thr			720
													gga Gly			768
													ttt Phe 270			816
													ttg Leu			864
													gag Glu			912
													aag Lys			960
													cat His			1008
													agc Ser 350			1056
													gca Ala			1104
			gjå aaa													1119

<210> 71 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS <222> (1)...(297) <223> HIV Protease <221> CDS <222> (298)...(1119) <223> Portion of HIV Reverse Transcriptase <400> 71 cct caa atc act ctt tgg caa cga ccc atc gtc tca ata aag ata ggg 48 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Ser Ile Lys Ile Gly ggg gca aat aaa gaa gct cta tta gat aca gga gca gat gat aca gta Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 96 tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg 144 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata 192 Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca 240 Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act 288 Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 90 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga 432 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt 480 Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc 528 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 200 gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg 672 Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220

aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat ccc gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val 275 280 285	864
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gcw agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Xaa Ser Gln 355 360 365	1104
att tat cca ggg att Ile Tyr Pro Gly Ile 370	1119
<210> 72 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (1)(297) <223> HIV Protease	
<221> CDS <222> (298)(1119) <223> Portion of HIV Reverse Transcriptase	
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ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96

												aaa Lys 45				144
												cag Gln				192
												ata Ile				240
												ctt Leu				288
												gta Val				336
												ttg Leu 125				384
												gaa Glu				432
												act Thr				480
												tta Leu				528
												gtt Val				576
												gta Val 205				624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttc Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aag Lys	gac Asp	ttc Phe	agg Arg	672
												gag Glu				720
												aaa Lys				768
												cct Pro				816
												gat Asp 285				864

Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cga cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Arg His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gag ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta caa cct ata gtg cta cca gag aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aag tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
ata tac gca ggg att Ile Tyr Ala Gly Ile 370	1119
<210> 73 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (1)(297) <223> HIV Protease	
.221. GDG	
<221> CDS <222> (298)(1119) <223> Portion of HIV Reverse Transcriptase	
<222> (298)(1119)	48
<222> (298)(1119) <223> Portion of HIV Reverse Transcriptase <400> 73 cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly	<b>4</b> 8 96
<pre>&lt;222&gt; (298)(1119) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 73 cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly 1</pre>	
<pre>&lt;222&gt; (298)(1119) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 73 cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly 1</pre>	96
<pre>&lt;222&gt; (298)(1119) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 73 cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly 1</pre>	96 144

tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gat Asp 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aaa Lys		336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu		384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	ctg Leu 140	gaa Glu	aag Lys	gaa Glu	gly aaa		432 ·
						cct Pro											480
						agt Ser											528
						act Thr											576
						tta Leu											624
						ttt Phe 215											672
						ata Ile											720
						gtg Val											768
						atg Met											816
						atc Ile											864
						999 Gly 295											912
						tgg Trp											960
						ctt Leu										1	.008
						ata Ile										1	.056

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg att Ile Tyr Pro Gly Ile 370	1119
<210> 74 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96 <sup>.</sup>
tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480

gct Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggt Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gtc Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
			gca Ala													720
			cag Gln													768
			caa Gln 260													816
			gac Asp													864
			tta Leu													912
			ctg Leu													960
			cct Pro													1008
			gta Val 340													1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att Ile	tat Tyr 370	gca Ala	gly ggg													1116
<211 <212	)> 75 .> 81 !> DN !> Hu	.9 IA	Immu	ınod∈	fici	.ency	. Vir	us (	HIV)							

<220>

<221> CDS <222> (1) ... (819) <223> Portion of HIV Reverse Transcriptase ccc att agt cct att gam act gta cca gta aaa tta aag cca gga atg Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys Pro Gly Met gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa aaa ata aaa 96 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys 25 gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca 144 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser aaa att ggg cct gaa aat cca tac aat act cca gta ttt gcc ata aag Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys 192 aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc aga gaa ctt Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu 240 aat aar aga act caa gat ttc tgg gaa gtt caa tta gga ata cca cat 288 Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His ecc tea ggg tta aaa aag aay aaa tea gta aca gta ttg gat gtg ggt 336 Pro Ser Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu Asp Val Gly 105 gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg aag tat act 384 Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg Lys Tyr Thr gca ttt acc ata cct agt ata aac aat gag aca cca ggg att agr tat 432 Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Xaa Tyr 135 cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc 480 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe caa agt agc atg aca aaa atc tta gag cct ttt aga aaa cat aat cca 528 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys His Asn Pro gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac 576 Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp 180 tta gaa ata gag gag cat aga aca aaa ata gag gaa ctg agr vrg cat 624 Leu Glu Ile Glu Glu His Arg Thr Lys Ile Glu Glu Leu Xaa Xaa His 195 200 ctg tta aag tgg gga ttt acy aca cca gac aaa aag cat cag aaa gaa 672 Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His Gln Lys Glu cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat aaa tgg aca Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr 720 230 235

										Ser					gac Asp	768
ata Ile	cag Gln	aag Lys	tta Leu 260	Val	gga Gly	aaa Lys	ttg Leu	aat Asn 265	Trp	gca Ala	agt Ser	cag Gln	att Ile 270	Tyr	gca Ala	816
GJ y aaa																819
<21 <21	0> 7 1> 8 2> D 3> H	19 NA	Imm	unode	efic	ienc	y Vi:	rus	(HIV	)						
<22 <22	1> C 2> ( 3> P	1) orti	.(81: on o:		/ Re	vers	e Tra	ansc.	ript	ase						
CCC	0> 7 att Ile	agt	cct Pro	att Ile 5	gaa Glu	act Thr	gta Val	cca Pro	gta Val 10	aaa Lys	tta Leu	aag Lys	cca Pro	gga Gly 15	atg Met	48
gat Asp	ggc Gly	cca Pro	aaa Lys 20	gty Xaa	aaa Lys	caa Gln	tgg Trp	cca Pro 25	tta Leu	aca Thr	gaa Glu	gaa Glu	aaa Lys 30	ata Ile	aga Arg	96
gca Ala	tta Leu	gta Val 35	gaa Glu	att Ile	tgt Cys	aca Thr	gaa Glu 40	atg Met	gaa Glu	aag Lys	gaa Glu	gga Gly 45	aaa Lys	att Ile	tca Ser	144
aaa Lys	att Ile 50	gj <sup>λ</sup> aaa	cct Pro	gaa Glu	aat Asn	cca Pro 55	tac Tyr	aat Asn	act Thr	cca Pro	gtg Val 60	ttt Phe	gct Ala	ata Ile	aag Lys	192
aaa Lys 65	aaa Lys	gac Asp	agt Ser	act Thr	aar Lys 70	tgg Trp	aga Arg	aaa Lys	ttg Leu	gta Val 75	gat Asp	ttc Phe	aga Arg	gaa Glu	ctt Leu 80	240
aat Asn	aag Lys	aga Arg	act Thr	caa Gln 85	gac Asp	ttc Phe	tgg Trp	gaa Glu	gtt Val 90	caa Gln	tta Leu	gga Gly	ata Ile	cca Pro 95	cat His	288
ccc Pro	tca Ser	ggg Gly	tta Leu 100	aaa Lys	aag Lys	aaa Lys	aaa Lys	tca Ser 105	gta Val	aca Thr	gta Val	ctg Leu	gat Asp 110	gtg Val	ggt Gly	336
gat Asp	gca Ala	tat Tyr 115	ttt Phe	tca Ser	gtt Val	ccc Pro	tta Leu 120	gat Asp	aaa Lys	gac Asp	ttc Phe	agg Arg 125	aag Lys	tat Tyr	act Thr	384
gca Ala	ttt Phe 130	act Thr	atn Xaa	cct Pro	agt Ser	ata Ile 135	aac Asn	aat Asn	gag Glu	Thr	cca Pro 140	gjå aaa	att Ile	agg Arg	tat Tyr	432
cag Gln 145	tac Tyr	aat Asn	gtg Val	Leu	cca Pro 150	caa Gln	gga Gly	tgg Trp	aaa Lys	gga Gly 155	tca Ser	cca Pro	gca Ala	ata Ile	ttc Phe 160	480

															cca Pro	528
									gat Asp							576
									ata Ile							624
ctg Leu	ttg Leu 210	agg Arg	tgg Trp	gga Gly	ttt Phe	acc Thr 215	aca Thr	cca Pro	gac Asp	aag Lys	aaa Lys 220	cat His	cag Gln	aaa Lys	gaa Glu	672
									ctc Leu							720
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									tgg Trp							816
gly ggg																819
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<222	.> CI !> (2 !> Pc	98).		-		rerse	e Tra	ansci	ripta	ıse						
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									aca Thr							96
	gaa								tgg							144
Leu	Ğlu	Asp 35	Met	Asn	Leu	Pro	40	Arg	Trp	Lys	Pro	45	мет	11e	GIÀ	

gaa Glu 65	atc Ile	tgc Cys	gga Gly	cat His	aaa Lys 70	gct Ala	gta Val	ggt Gly	aaa Lys	gta Val 75	tta Leu	gta Val	gga Gly	cct	aca Thr 80	240
					Gly							ctt Leu				288
												gta Val			aag Lys	336
												ttg Leu 125				384
												gag Glu				432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
												tta Leu				528
												gtt Val				576
nnn Xaa	nnn Xaa	nnn Xaa 195	nnn Xaa	nnn Xaa	61 <sup>3</sup>	twa Xaa	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gta Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttc Phe 215	tca Ser	gtt Val	cct Pro	cta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	aga Arg	672
aag Lys 225	tac Tyr	act Thr	gca Ala	ttc Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctg Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gtg Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ttg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
ata tat gca ggg Ile Tyr Ala Gly 370	1116
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<pre>&lt;400&gt; 78 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1 5 10 15</pre>	48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384

aaa Lys	ata Ile 130	aaa Lys	gca Ala	ttg Leu	gta Val	gaa Glu 135	ata Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	gjå aaa	432	
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	acr Xaa	cca Pro	gta Val	ttt Phe 160	480	
gcc Ala	ata Ile	arg Xaa	aaa Lys	aaa Lys 165	gaa Glu	agc Ser	tct Ser	agc Ser	tct Ser 170	aaa Lys	tgg Trp	aga Arg	aaa Lys	tta Leu 175	gta Val	528	
gat Asp	ttc Phe	aga Arg	gaa Glu 180	ctt Leu	aat Asn	aar Lys	aga Arg	act Thr 185	caa Gln	gac Asp	ttt Phe	ttk Xaa	gaa Glu 190	gtt Val	caa Gln	576	
tta Leu	gga Gly	ata Ile 195	cca Pro	cat His	ccc Pro	gca Ala	999 Gly 200	tta Leu	aag Lys	aag Lys	aaa Lys	aaa Lys 205	tca Ser	gya Xaa	aca Thr	624	
rta Xaa	ttg Leu 210	gat Asp	gtg Val	ggt Gly	gat Asp	gca Ala 215	tat Tyr	ttt Phe	tca Ser	gtt Val	ccc Pro 220	tta Leu	gat Asp	raa Xaa	gac Asp	672	
ttc Phe 225	agg Arg	aag Lys	tat Tyr	act Thr	gca Ala 230	ttt Phe	acc Thr	ata Ile	cct Pro	agt Ser 235	ata Ile	aac Asn	aat Asn	gag Glu	aca Thr 240	720	
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tca Ser	cca Pro	gct Ala	ata Ile 260	ttc Phe	caa Gln	agt Ser	agc Ser	atg Met 265	aca Thr	aaa Lys	atc Ile	tta Leu	gag Glu 270	cct Pro	ttt Phe	816	
aga Arg	aaa Lys	caa Gln 275	aat Asn	cca Pro	gay Asp	ata Ile	gtt Val 280	atc Ile	tat Tyr	caa Gln	tac Tyr	atg Met 285	gat Asp	gat Asp	ttg Leu	864	
tat Tyr	gta Val 290	gga Gly	tct Ser	gay Asp	tta Leu	gaa Glu 295	ata Ile	gag Glu	cag Gln	cat His	aga Arg 300	ata Ile	aaa Lys	ata Ile	gag Glu	912	
gaa Glu 305	ctg Leu	aga Arg	caa Gln	yat Xaa	ytg Xaa 310	tgg Trp	arg Xaa	tgg Trp	ggr Xaa	ttt Phe 315	tac Tyr	aca Thr	cca Pro	gac Asp	aaa Lys 320	960	
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cct Pro	gat Asp	aaa Lys	tgg Trp 340	aca Thr	gta Val	cag Gln	cct Pro	ata Ile 345	gtg Val	ctg Leu	cca Pro	gaa Glu	aaa Lys 350	gac Asp	agc Ser	1056	
tgg Trp	act Thr	gtc Val 355	aat Asn	gac Asp	ata Ile	cag Gln	aag Lys 360	tta Leu	gtg Val	gga Gly	aaa Lys	ttg Leu 365	aat Asn	tgg Trp	gca Ala	1104	
			tat Tyr													1122	

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<220>
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<223> HIV Protease
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ggg caa cta aag gaa gct cta tta gat aca gga gca gac aat aca gta
                                                                           96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val
ttc gaa gac ctg gat tta cca gga agg tgg aaa cca aaa atg ata ggg
                                                                          144
Phe Glu Asp Leu Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
gga att gga ggt ttt atc aaa gta aaa cag tat gag cag ata ccc ata
                                                                          192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Pro Ile
                          55
gaa atc tgt ggg cgt aaa gct ata ggt aca gtg tta gta gga cct aca
                                                                          240
Glu Ile Cys Gly Arg Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
ect gte aac ata att gga aga gat etg ttg act cag att ggt tge act
                                                                          288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
                                                                          336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa
                                                                          384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                              120
aaa ata aaa gca tta ata gaa att tgt gca gaa atg gaa aag gaa ggg
                                                                          432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Ala Glu Met Glu Lys Glu Gly
    130
                          135
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt
                                                                          480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145
                                                                160
gcc ata aag aaa aag aac agt aat aaa tgg aga aaa tta gta gat ttc
                                                                          528
Ala Ile Lys Lys Lys Asn Ser Asn Lys Trp Arg Lys Leu Val Asp Phe
                 165
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                                                          576
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624
ata cca cat ccc gca ggg tta aaa aag aaa aag tca ata aca gta tta
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Ile Thr Val Leu
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
                                                                             672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg
                                                                             720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                                                             768
                  245
                                        250
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa
                                                                             816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
             260
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta
                                                                            864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               280
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg
                                                                            912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu
aga caa cat ctg ttg agg tgg gga ctt acc aca cca gac cag aaa cat
                                                                            960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Gln Lys His
                     310
                                            315
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat
                                                                           1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
aaa tgg aca gta cag cct ata gtg ctg cca gac aaa gac agc tgg act
                                                                           1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr
gtc aat gac ata cag aag tta gtg ggr aaa ttg aat tgg gca agt caa
                                                                           1104
Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Leu Asn Trp Ala Ser Gln
att tac cca ggg
                                                                           1116
Ile Tyr Pro Gly
    370
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<223> HIV Protease
<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase
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pro Gin II		5	GIII AI	g FIO	10	Val	1112	110	_70	15	1	
ggg cag ct Gly Gln Le	a aag g u Lys G 20	ag gct lu Ala	cta tt Leu Le	a gat u Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
tta gaa ga Leu Glu Gl 3	u Met A	at ttg sn Leu	Pro Gl	a aga y Arg 0	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	Gly aaa	144
gga att gg Gly Ile Gl 50	a ggt t y Gly P	tt atc he Ile	aaa gt Lys Va 55	a aga l Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	ctc Leu	ata Ile	192
gaa att tg Glu Ile Cy 65	t gga c s Gly H	at aaa is Lys 70	gct at Ala Il	a ggt e Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct gtc aa Pro Val As	n Ile I	tt gga le Gly 85	aga aa Arg As	t ctg n Leu	ttg Leu 90	acw Xaa	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta aat tt Leu Asn Ph	t ccc a e Pro I 100	tt agt le Ser	cct at Pro Il	t gaa e Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca gga at Pro Gly Me 11	t Asp G	gc cca ly Pro	aga gt Arg Va 12	l Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa ata aa Lys Ile Ly 130												432
aaa att tc Lys Ile Se 145	a aaa a r Lys I	tt ggg le Gly 150	cct ga Pro Gl	a aat u Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	rta Xaa	ttt Phe 160	480
gcc ata aa Ala Ile Ly	s Lys L	aa gac ys Asp 65	agt ac Ser Th	t aaa r Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga gaa ct Arg Glu Le	t aat a u Asn L 180	ag agg ys Arg	act ca Thr Gl	a gat n Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata cca ca Ile Pro Hi 19	s Pro A	ca ggg la Gly	ttg aa Leu Ly 20	s Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat gtg gg Asp Val Gl 210	t gat g y Asp A	ca tat la Tyr	ttc tc Phe Se 215	a gtt r Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	aga Arg	672
aag tat ac Lys Tyr Th 225												720
att aga ta Ile Arg Ty	r Gln T	ac aat yr Asn 45	gtg ct Val Le	t cca u Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
					-136	-						

			caa Gln 260													816
			gac Asp													864
			tta Leu													912
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			cct Pro													1008
			gtg Val 340													1056
			ata Ile													1104
			G1y 999													1119
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\Z.I.	3> Hu	ıman	Immu	node	fici	ency	. Vir	rus	HIV)							
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<220 <221 <222 <223 <222 <223 <400 cct	)> L> CE 2> (1 3> H1 L> CE 2> (2 3> Pc 0> 81	OS V Pr OS (98). Ortic	(297 cotea (1	) se 116) HIV	' Rev	erse	: Tra	nscr	ripta	gtt	rcc Xaa	ata Ile	aag aag	ata Ile 15	ggg ggg	48
<220 <221 <222 <223 <223 <400 cct Pro 1	)> L> CL 2> (1 3> H1 L> CL 2> (2 3> Pc )> 81 caa Gln	OS (V Pr (S) (S) (S) (S) (S) (S) (S) (S) (S) (S)	(297 Totea (1 on of	116) HIV ctt Leu 5	' Rev tgg Trp gct	erse caa Gln cta	: Tra cga Arg tta	inscr ccy Xaa gat	ctt Leu 10 aca	gtt Val gga	Xaa gca	Ile gat	Lys gat	Ile 15 aca	Gly gta	48 96
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gaa Glu 65	att Ile	tgt Cys	gga Gly	cat His	aga Arg 70	gct Ala	ata Ile	ggt Gly	aca Thr	gtw Xaa 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	24	40
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	agr Xaa	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	2	88
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	33	36
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	3	84
aaa Lys	ata Ile 130	aaa Lys	gca Ala	ttg Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	gga Gly	43	32
aaa Lys 145	att Ile	tca Ser	aga Arg	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	4	80
gct Ala	ata Ile	aag Lys	aaa Lys	aar Lys 165	gat Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	5:	28
agg Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	agg Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	5′	76
					Gly aaa											62	24
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	6.	72
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	act Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	72	20
att Ile	aga Arg	tat Tyr	caa Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	76	68
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cca Pro	ttt Phe 270	aga Arg	aaa Lys	8:	16
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtc Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	86	64
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gga Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	yta Xaa	9:	12
					arg Xaa 310											9(	60

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008											
aaa tgg aca gta cag cct ata cag ctg cca gaa aag gaa agc tgg act Lys Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056											
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104											
att tat gca ggg Ile Tyr Ala Gly 370	1116											
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ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96											
tta gaa gaa atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144											
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val 50 55 60	192											
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240											
ccc gtc aac ata att gga aga aat ctg ttg act cag att ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95.	288											
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336											
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384											

		Lys													gly	432
	Ile		aaa Lys													480
			aag Lys													528
			aay Asn 180												gga Gly	576
			ccc Pro												ctg Leu	624
			gat Asp													672
aar Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	gta Val	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttt Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tay Tyr 280	cag Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggr Xaa 295	aag Lys	cac His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gag Glu	cta Leu	912
aga Arg 305	cag Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctk Xaa	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	aaa Lys	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gty Xaa	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	Leu	gtg Val 360	gga Gly	aaa Lys	ttr Xaa	aat Asn	tgg Trp 365	gcc Ala	agt Ser	cag Gln	1104
	tat Tyr 370															1116

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<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta
                                                                          96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
tta gaa gac atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg
                                                                         144
Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata
                                                                         192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca
                                                                         240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act
                                                                         288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
                                                                         336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa
                                                                         384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                             120
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga
                                                                         432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt
                                                                         480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
gcc ata aag aaa aaa gac agt act aaa tgg agg aaa tta gta gat ttt
                                                                         528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                                                                         576
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
            180
                                 185
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ata cca cat cca gca ggg tta aaa aag aaa aag tca gta aca gtg ctg
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
                                                                                         624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
                                                                                         672
aag tat act gca ttt acc ata ccc agt ata aac aat gag aca ccc agg
                                                                                         720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Arg
                          230
gtt aga tat caa tac aat gta ctt cca cag gga tgg aaa gga tca cca
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                                                                         768
gca tat ttc caa agt agc atg aca aaa atc tta gaa ccc ttc aga aaa Ala Tyr Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                                                                                         816
caa aac cca gac ata gtt atc tat caa tac atg gat gac tta tat gta {
m Gln} Asn {
m Pro} Asp {
m Ile} Val {
m Ile} Tyr {
m Gln} Tyr Met Asp Asp {
m Leu} Tyr {
m Val}
                                                                                         864
gga tot gac tta gag ata gga cag cat aga gca aaa ata gag gac cta
                                                                                         912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Asp Leu
aga gca cat ctg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat
                                                                                         960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
                         310
                                                   315
cag aaa gaa ccc cca ttt ctc tgg atg ggt tat gaa ctc cat cct gat
                                                                                       1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
aaa tgg aca gta cag cct ata gwg cta cca gaa aaa gac agc tgg act
                                                                                       1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr
               340
gtc aat gac ata cag aaa tta gta gga aaa tta aat tgg gca agt cag
                                                                                       1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
att tat cca ggg
                                                                                       1116
Ile Tyr Pro Gly
     370
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<220>
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<222> (1)...(297)
<223> HIV Protease
<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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ggg caa cta Gly Gln Leu	atg gaa Met Glu 20	gct cta Ala Leu	tta gat Leu Asp 25	aca gga Thr Gly	gca gat Ala Asp	gat Asp 30	aca Thr	gta Val	96
tta gaa gac Leu Glu Asp 35	ata aat Ile Asn	ttg cca Leu Pro	gga aga Gly Arg 40	tgg aaa Trp Lys	cca aaa Pro Lys 45	ata Ile	ata Ile	gj <sup>λ</sup> aaa	144
gga att ggt Gly Ile Gly 50	ggt ttt Gly Phe	gtc aaa Val Lys 55	gtg aga Val Arg	cag tat Gln Tyr	gat cag Asp Gln 60	gta Val	ccc Pro	ata Ile	192
gaa atc tgt Glu Ile Cys 65	gga cat Gly His	aaa gtt Lys Val 70	ata ggt Ile Gly	aca gta Thr Val 75	tta gta Leu Val	gga Gly	cct Pro	aca Thr 80	240
cct acc aac Pro Thr Asn	gta gtt Val Val 85	gga aga Gly Arg	aat ctg Asn Leu	atg act Met Thr 90	cag att Gln Ile	ggc Gly	tgc Cys 95	acy Xaa	288
tta aat ttt Leu Asn Phe									336
cca gga atg Pro Gly Met 115									384
aaa ata aaa Lys Ile Lys 130									432
aaa att tca Lys Ile Ser 145									480
gcc ata aag Ala Ile Lys									528
aga gaa ctt Arg Glu Leu									576
ata cca cat Ile Pro•His 195									624
gat ata ggt Asp Ile Gly 210			_		-	-			672
aag tat act Lys Tyr Thr 225									720
gtt aga tat Val Arg Tyr									768

		c caa ne Glr 260	ı Ser										Arg		816
cag a Gln A	Asn P	ca gad co Asp 75	ata Ile	gtt Val	atc Ile	tgc Cys 280	Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
Gly S		ac tta sp Leu													912
		at ct <u>c</u> aa Lev													960
		a cct u Pro													1008
aaa t Lys T		a gta ır Val 340	Gln												1056
gtc a Val A	at ga sn As 35	p Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att t Ile T 3															1116
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ggg ca	aa ct ln Le	a aag u Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
tta ga Leu G	aa ga lu Gl 3	u Met	aat Asn	ttg Leu	cca Pro	999 Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	gly ggg	144

			gga Gly													240
			ata Ile							Thr						288
			ccc Pro 100													336
			gat Asp													384
			gca Ala													432
			aaa Lys													480
			aaa Lys													528
			aat Asn 180													576 <sup>.</sup>
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly aaa	tta Leu	aaa Lys 200	aag Lys	aam Xaa	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gay Asp	gtg Val 210	ggt Gly	gat Asp	gcr Xaa	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ссу Хаа	tta Leu	gay Asp 220	aaa Lys	gay Asp	ttc Phe	agg Arg	672
			gca Ala													720
			cag Gln													768
			caa Gln 260													816
			gac Asp													864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gga Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	cag Gln 310	tgg Trp	G1 Y 999	tta Leu	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960

cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat ccg gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata wtg ctg cca gac aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Asp Lys Asp Ser Trp Thr 340 345 350	1056
gtm aat gac ata cag aar tta gta gga aaa ttg aat tgg gcg agt cag Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
atc tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg cac aca acg gaa gct cta tta gat aca gga gca gat gat aca gta Gly His Thr Thr Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata gga Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile 50 55 60	192
gaa ttc tgt gga cat aaa act gta ggt aca gta tta ata gga cct aca Glu Phe Cys Gly His Lys Thr Val Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg atg act cag att ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggg ccc aaa gtt aaa cca tgg cca ttg aca gaa aga Pro Gly Met Asp Gly Pro Lys Val Lys Pro Trp Pro Leu Thr Glu Arg 115 120 125	384

															agg Arg	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gag Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
															ttc Phe	528
															gga Gly	576
															ctg Leu	624
						ttt Phe 215										672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttc Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gaa Glu	aca Thr	cca Pro	999 Gly 240	720
						gtg Val										768
						atg Met										816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tgt Cys 280	cag Gln	tac Tyr	atg Met	gat Asp	gac Asp 285	ttg Leu	tat Tyr	gta Val	864
						999 Gly 295										912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gjà aaa	ttt Phe	ttc Phe	aca Thr 315	cca Pro	gac Asp	gaa Glu	aaa Lys	cat His 320	960
						ctt Leu										1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gta Val	ctg Leu 345	cca Pro	gac Asp	caa Gln	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
						tta Leu										1104
		cca Pro														1116

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<223> HIV Protease
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                                                                                       48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                                                                                       96
                                                                                      144
tta gaa gaa atg aat ttg tca gga aga tgg aaa cca aaa atg ata ggg
Leu Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
                                                                                      192
                              55
gag atc tgt gga cat aaa gct gta ggt aca gta tta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
                                                                                      240
                                                                                      288
cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc acc
Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
                                                                                      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa
                                                                                      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                                  120
                                                           125
                                                                                      432
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
    130
                             135
                                                                                      480
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat tty
                                                                                      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                   165
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                                                                      576
              180
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ata cca cat ccy gca ggg ttg aar aag aaa aaa tca gta aca gta ctg
Ile Pro His Xaa Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                                                                                    624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gay ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
                                                                                   672
                                                                                   720
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
gtt aga tat car tac aat gtg ctt cca cag gga tgg aag gga tca cca
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                                                                   768
                   245
                                           250
gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt agg aaa
                                                                                   816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
              260
caa aat cca gat ata gtt atc tat caa tac atg gat gac ttr tat gta
                                                                                   864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val
gga tot gao tta gaa ata ggg car cat aga aca aaa ata gag gaa ttg
                                                                                   912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
aga caa cat ctg ttg aag tgg gga tta acc aca cca gac aaa aaa cat
                                                                                   960
Arg Gln His Leu Leu Lys Trp Gly Leu Thr Thr Pro Asp Lys Lys His
                       310
                                                315
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                                                                  1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act
                                                                                  1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt cag
                                                                                  1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
att tat gca ggg
                                                                                  1116
Ile Tyr Āla Gly
    370
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<223> Portion of HIV Reverse Transcriptase
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					gct Ala											96
					ttg Leu											144
					gtc Val											192
					aaa Lys 70											240
					gga Gly											288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	aaa Lys	gaa Glu	384
					atr Xaa											432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	ccg Pro	tac Tyr 155	aac Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gga Gly	ggt Gly	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	ata Ile	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aaa Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
					gjå aaa											624
					tat Tyr											672
					act Thr 230											720
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gca ata ttt caa agt agc atg aca aaa atc tta gag ccc ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc twt caw tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Xaa Xaa Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg aag cat agg gaa aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Lys His Arg Glu Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac gaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Glu Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ctt gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Leu Asp 325 330 335	1008
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg agt ttg cca ggg aga tgg aaa cca aaa atg ata ggg	
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144

								ggt Gly							aca Thr 80	240
								ctg Leu								288
								gaa Glu 105								336
								aaa Lys								384
								tgt Cys								432
								aat Asn								480
								aaa Lys								528
								gac Asp 185								576
								aag Lys								624
								gtt Val								672
aaa Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
								cca Pro								768
gca Ala	ata Ile	ttt Phe	caa Gln 260	cat His	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
cag Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gac Asp 285	ttg Leu	tat Tyr	gta Val	864
								cat His								912
								ttt Phe								960

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aac ttg cca gga aaa tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384

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aag Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
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aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
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gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttc Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
					acc Thr 230											720
					aat Asn											768
					agc Ser											816
					gtt Val											864
gga Gly	tct Ser 290	gat Asp	tta Leu	gaa Glu	ata Ile	gar Glu 295	cag Gln	cay His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
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					ttc Phe											1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cat His	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
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<223> HIV Protease
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta
                                                                          96
Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                                                                         144
ttg gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa ata ata ggg
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
                                                                         192
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
gaa atc tgt gga cat aaa gtt ata rgt cca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Val Ile Xaa Pro Val Leu Ile Gly Pro Thr
                                                                         240
                                                                         288
cct gtc aac ata att gga aga aat ttg atg act cag att ggc tgc act
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
tta aat ttt ccc atc agt cct att raa act gta cca gta aaa tta aag
                                                                         336
Leu Asn Phe Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys
                                  105
cca gga atg gat ggc cca aag gtt aaa caa tgg cca ttg aca gaa gaa
                                                                         384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                             120
                                                                         432
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                         135
                                                                         480
aaa atc tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145
gcc ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc
                                                                         528
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
                                                                         576
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga
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624
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Ile Pro His Pro Gly Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
gat gtg ggt gat gca tat ttt tca gtt cct cta gat gaa gac ttc agg
                                                                          672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
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Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
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                 245
gca ata ttt cag gct agc atg aca aaa atc tta gag ccg ttt aga aaa
                                                                         816
Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                                  265
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta
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Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
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gga tct gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg
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Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
aga caa cat ttg ttg aaa tgg gga ttt atc aca cca gat gaa aaa cat
                                                                         960
Arg Gln His Leu Leu Lys Trp Gly Phe Ile Thr Pro Asp Glu Lys His
                                          315
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                                                        1008
aag tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act
                                                                        1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
            340
                                  345
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag
                                                                        1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
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Ile Tyr Ala
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												aaa Lys 45				144
												cag Gln				192
												gta Val				240
												att Ile				288
		_		_	_			_		_		gta Val			_	336
		_	_									ttg Leu 125		-	_	384
												gaa Glu				432
												act Thr				480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	aac Asn	agt Ser	act Thr	aga Arg	tgg Trp 170	aga Arg	aaa Lys	gta Val	gta Val	gat Asp 175	ttc Phe	528
												gtt Val				576
												gta Val 205				624
												gaa Glu				672
												gag Glu				720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768

			caa Gln 260													816
caa Gln	aat Asn	cca Pro 275	gac Asp	ctg Leu	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	tta Leu	tat Tyr	gta Val	864
			cta Leu													912
agg Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	gaa Glu	aaa Lys	cat His 320	960
			cct Pro													1008
		_	gta Val 340			_		_		_		_	_		_	1056
			ata Ile													1104
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gaa Glu 65	atc Ile	tgc Cys	Gly 999	cat His	aaa Lys 70	gct Ala	gta Val	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gcc Ala	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggc Gly	tgt Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gat Asp 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	ara Xaa	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gag Glu	384
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					gly aaa											624
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					aat Asn											768
					agc Ser											816
					rtt Xaa											864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gag Glu 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gat Asp	gaa Glu	ctg Leu	912
aga Arg 305	gac Asp	cat His	ctg Leu	tgg Trp	aag Lys 310	tgg Trp	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aac Asn	aaa Lys	yat Xaa 320	960

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gtc Val			ata Ile													1104
Asn		gca Ala														1116
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	> CI > (3	L)	. (297 rotea													
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999 999																96
tta ( Leu																144
gga Gly																192
gaa Glu 65																240
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tta a Leu a		_		_	_		_		_	_		_			_	336
cca ( Pro (																384

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aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gjå aaa	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gly ggg	tta Leu	cca Pro 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
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gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	acc Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg
                                                                                  144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc gta
                                                                                  192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Val
gaa atc tgt ggr cat aaa gct ata ggt aca gta tta rta gga cct aca
                                                                                  240
Glu Ile Cys Xaa His Lys Ala Ile Gly Thr Val Leu Xaa Gly Pro Thr
cct gtc aac ata att gga agg aat ttg ttg act cag att ggt tgc act
                                                                                  288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
                                                                                  336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa
                                                                                  384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                                 120
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                                                                                  432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                                                                                  480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc
                                                                                  528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
aga gaa ctt aat aag aaa act caa gac ttt tgg gar gtt caa tta gga
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
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gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672											
aag tac act gca ttt act ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 235 230 235 240	720											
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Gly 999	caa Gln	cta Leu	agg Arg 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val		96
tta Leu	gaa Glu	gaa Glu 35	ata Ile	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	gly ggg		144
gga Gly	att Ile 50	Gly 999	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	sag Xaa	tat Tyr	gat Asp 60	cag Gln	gta Val	ccc Pro	gta Val		192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	ccc Pro	aca Thr 80		240
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tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	ara Xaa 110	tta Leu	aag Lys	•	336
cca Pro	ggr Xaa	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu		384
	ata Ile 130																432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	ata Ile	ttt Phe 160		480
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agg Arg	gaa Glu	ctc Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	ggm Xaa		576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	Gly 999	ttg Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gtr Xaa 205	aca Thr	gta Val	ctg Leu		624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gaa Glu	ttc Phe	agg Arg		672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	gta Val	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240		720
atc Ile	aga Arg	tat Tyr	caa Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aag Lys	gga Gly	tca Ser 255	cca Pro		768

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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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<pre>&lt;213&gt; Human Immunodeficiency Virus (HIV)  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(297) &lt;223&gt; HIV Protease  &lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 97 cct caa atc act ctt tgg caa cga ccc ctc gtc aaa ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Lys Ile Gly</pre>	<b>4</b> 8 96
<pre>&lt;213&gt; Human Immunodeficiency Virus (HIV)  &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)(297) &lt;223&gt; HIV Protease  &lt;221&gt; CDS &lt;222&gt; (298)(1116) &lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 97 cct caa atc act ctt tgg caa cga ccc ctc gtc aaa ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Lys Ile Lys Ile Gly 1 5 10 15  ggg caa ata aag gaa gcy tta tta gat aca gga gca gat gat aca gtg Gly Gln Ile Lys Glu Xaa Leu Leu Asp Thr Gly Ala Asp Asp Thr Val</pre>	

			aaa Lys 70								240
			gga Gly								288
			agt Ser								336
			cca Pro								384
			cta Leu								432
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			aga Arg								576
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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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tta gaa gaa atg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	192
gaa aty tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384

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Leu Glu Glu Met Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
                                                                                  144
                                                                                  192
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Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Leu
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cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                                                                                  288
                    85
tta aat ttt ccc att agt cct att gaa act gta cct gta aaa tta aag
                                                                                  336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa
                                                                                  384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                                 120
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg
                                                                                  432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc
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Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
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Ile Pro His Pro Ser Gly Leu Xaa Lys Lys Lys Ser Val Thr Val Leu
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
                      230
                                                                            768
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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
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                                       250
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Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
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Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val
rgc tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg
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Xaa Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
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Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                                                           1008
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
             340
                                                                           1104
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aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
								aaa Lys								528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
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								agt Ser								720
								cca Pro								768

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gga tct gac t Gly Ser Asp L 290	ta gaa a Leu Glu I	ata ggg Ile Gly 295	cag Gln	cat H <b>i</b> s	aga Arg	gca Ala	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga caa cat c Arg Gln His L 305	Leu Trp <i>l</i>	agg tgg Arg Trp 310	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag aag gaa c Gln Lys Glu P	cct cca t Pro Pro 1 325	ttc ctt Phe Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
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gtc aat gam a Val Asn Xaa I 355	ata cag a Ile Gln 1	aaa tta Lys Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn	tgg Trp 365	gcc Ala	agt Ser	cag Gln	1104
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cct car atc a Pro Gln Ile I  1 ggr cag vta a	Thr Leu 5  aag gaa Lys Glu 20  atg tat	Trp Gln gct tta Ala Leu ttg cca	Thr tta Leu gga	Pro gay Asp 25 aga	Leu 10 aca Thr	Val gra Xaa aaa	yca Ala cca	gat Asp	gat Asp 30	Xaa 15 mca Xaa ata	gta Val	

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tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	tct Ser	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aga Arg 110	tta Leu	aag Lys	336
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ggg caa cta aag gaa gct cta ttg gat aca gga gca gat gat aca ata Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile 20 25 30	96
tta gaa gaa atg tgt ttg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly 130 135 140	432

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aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145
                        150
gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta qta qat ttc
                                                                                     528
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe
                   165
                                            170
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg
                                                                                     624
Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu
                                  200
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga
                                                                                     672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg
                                                                                     720
Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly
                        230
att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca
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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag
                                                                                     816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                                       265
caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val
                                                                                     864
gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu
                                                                                     912
    290
aga caa tat ctg tgg gag tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
                                                                                     960
caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat Gln Gln Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                                                                   1008
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp
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<223> HIV Protease

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														aca Thr		96
														ata Ile		144
														ccc Pro		192
														cct Pro		240
ccg Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ctg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	aba Xaa	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggr Xaa	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	ccg Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aaa Lys	act Thr	caa Gln	gac Asp 185	ttt Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cac His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
														ccc Pro		720

att aga tat Ile Arg Tyr	cag tac Gln Tyr 245	aat gtg Asn Val	ctt cca Leu Pro	cag gg Gln Gl <sub>y</sub> 250	a tgg a y Trp I	aaa gga Lys Gly	tcg cca Ser Pro 255	768
gca ata ttc Ala Ile Phe	caa agt Gln Ser 260	agc atg Ser Met	aca aaa Thr Lys 265	Ile Le	a gag c ı Glu E	ect ttt Pro Phe 270	aga aaa Arg Lys	816
caa aat cca Gln Asn Pro 275	gac ata Asp Ile	gtt atc Val Ile	tat caa Tyr Gln 280	tat gto	l Asp A	gat ttg Asp Leu 285	tat gta Tyr Val	864
gga tct gac Gly Ser Asp 290	tta gag Leu Glu	ata ggg Ile Gly 295	cag cat Gln His	aga aca Arg Thi	a aaa a r Lys I 300	ata gag [le Glu	gaa ctg Glu Leu	912
aga saa cat Arg Xaa His 305					r Pro Ā			960
cag aaa gaa Gln Lys Glu								1008
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ggg caa tta Gly Gln Leu								96
cta gaa gaa Leu Glu Glu 35					Pro L			144

gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	car Gln	ata Ile	cyt Xaa	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttr Xaa 90	act Thr	cag Gln	att Ile	ggc Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	ata Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
														gaa Glu		384
														gaa Glu		432
														gta Val		480
														gat Asp 175		528
														tta Leu		576
														gta Val		624
														ttc Phe		672
														ccg Pro		720
														tca Ser 255		768
gcc Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	att Ile	tta Leu	gat Asp	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
														tat Tyr		864
														gaa Glu		912

Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
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														gaa Glu			384
														gaa Glu			432
aar Lys 145	att Ile	tca Ser	aaa Lys	att Ile	999 Gly 150	cct Pro	gaa Glu	aac Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160		480
														gat Asp 175			528
														tta Leu			576
														gta Val			624
														ttc Phe			672
														cca Pro			720
														tca Ser 255			768
														aga Arg			816
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gga Gly	tct Ser 290	gat Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu		912
aga Arg 305	car Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aar Lys	cat His 320		960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1	800
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aag Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1	056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1	104

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ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val 20 25 30	96												
tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Xaa Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144												
gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata gtt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Val Val 50 55 60	192												
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240												
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288												
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336												
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gag gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384												
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aaa att tca aaa aty ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Xaa Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480												
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528												

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ata cca cat c Ile Pro His I 195	ccc gca ( Pro Ala (	ggg yta Gly Xaa	aaa a Lys L 200	ag aac ys Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat gtg ggt g Asp Val Gly A 210	gat gca Asp Ala '	tat ttc Tyr Phe 215	tca g Ser V	tt ccc al Pro	Leu	gat Asp 220	aaa Lys	gac Asp	ttt Phe	agg Arg	672
aag tat act g Lys Tyr Thr A 225	Ala Phe'	acc ata Thr Ile 230	ccc as	gt ata er Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att aga tat o Ile Arg Tyr G											768
gca ata ttc c Ala Ile Phe c			Thr Ly								816
caa aat cca g Gln Asn Pro A 275											864
gga tct gac t Gly Ser Asp I 290					Thr						912
aga gca cat c Arg Ala His I 305	Leu Leu :										960
cag aaa gaa c Gln Lys Glu F											1008
aaa tgg aca g Lys Trp Thr V 3			Lys L								1056
gtc aat gat a Val Asn Asp I 355	ata cag a Ile Gln I	aag tta Lys Leu	gtg gg Val G 360	ga aaa ly Lys	ttg Leu	aat Asn	tgg Trp 365	gcc Ala	agt Ser	cag Gln	1104
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gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat cag tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cac aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca ggg aaa tgg aag cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144

					atc Ile											192
					aaa Lys 70											240
					gga Gly											288
					agt Ser											336
					cca Pro											384
					gta Val											432
					999 Gly 150											480
gct Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	cct Pro	gca Ala	ggt Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	cta Leu	624
gat Asp	gtg Val 210	G1y 999	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	aac Asn	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gta Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	tgt Cys	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttc Phe 270	aga Arg	aag Lys	816
caa Gln	aat Asn	cca Pro 275	gaa Glu	atg Met	gtt Val	atc Ile	trc Xaa 280	caa Gln	tac Tyr	gtg Val	gat Asp	gay Asp 285	ttg Leu	tat Tyr	gta Val	864
ggt Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	999 Gly 295	cag Gln	cat His	aga Arg	gca Ala	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctr Xaa	912

305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctm cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Xaa His Pro Asp 325 330 335	1008
aaa tgg aca gtg cag cat ata gaa ctg cca gaa caa gag agc tgg act Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Gln Glu Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa yta aat tgg gca agy cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Xaa Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
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<400> 109 cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu	48 96
<pre>&lt;400&gt; 109 cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu 1</pre>	
<pre>&lt;400&gt; 109 cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu 1</pre>	96
<pre> &lt;400&gt; 109 cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu 1</pre>	96
<pre>ct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu 1</pre>	96 144 192

cas	aaa	ata.	ant	~~~	~~~		~++									201
					cca Pro											384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	ttg Leu 140	gaa Glu	aag Lys	gaa Glu	gga Gly	432
					999 Gly 150											480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
					aga Arg											576
					Gly ggg											624
					tat Tyr											672
					nnn Xaa 230											720
					nnn Xaa											768
					agc Ser											816
					gtt Val											864
					ata Ile											912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
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att tat cca ggg Ile Tyr Pro Gly 370	1116												
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<pre>&lt;400&gt; 110 cyt cag atc act ctt tgg caa cga ccc cts gtc aca ata aag gta ggg Xaa Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly 1 5 10 15</pre>	48												
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96												
tta gaa gaa atr aat ttg cca ggr aaa tgg aaa cca awa atg ata ggg Leu Glu Glu Xaa Asn Leu Pro Xaa Lys Trp Lys Pro Xaa Met Ile Gly 35 40 45	144												
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile 50 55 60	192												
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240												
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288												
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336												
cca ggg atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384												
aaa ata aaa gca tta ata gaa atc tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432												
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480												
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528												

aga gaa ctt aat Arg Glu Leu Asn 180											576
ata cca cat ccc Ile Pro His Pro 195											624
gat gtg ggt gat Asp Val Gly Asp 210											672
aag tac act gca Lys Tyr Thr Ala 225											720
att aga tat cag Ile Arg Tyr Gln											768
gca ata ttc caa Ala Ile Phe Gln 260	agt agc Ser Ser	atg aca Met Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa mat cca gac Gln Xaa Pro Asp 275											864
gga tct gac tta Gly Ser Asp Leu 290											912
aga cag cat ttg Arg Gln His Leu 305	ttg aag Leu Lys 310	tgg gga Trp Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aag Lys	cat His 320	960
cag aaa gag cct Gln Lys Glu Pro											1008
aaa tgg aca gta Lys Trp Thr Val 340	cag cct Gln Pro	ata gag Ile Glu	ctg Leu 345	cca Pro	gaa Glu	aar Lys	gam Xaa	agc Ser 350	tgg Trp	act Thr	1056
gtc aat gac ata Val Asn Asp Ile 355	cag aaa Gln Lys	ata gtg Ile Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att tac cca ggg Ile Tyr Pro Gly 370											1116
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<220> <221> CDS <222> (1)(297 <223> HIV Protea	•										

<221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase <400> 111 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta 96 Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val tta gaa gaa atg agc ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 144 gga att gga ggt ttt atc aaa gta agm cag tat gwt cat ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Xaa His Ile Pro Ile 192 gaa wtc tgt ggm cat aaa gct gaa ggt aca gta tta ata gga cct aca Glu Xaa Cys Xaa His Lys Ala Glu Gly Thr Val Leu Ile Gly Pro Thr 240 288 cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 336 tta aat ttt ccc ata agt cct att gaa act gta cca gta aga cta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Arg Leu Lys 100 105 cca gga atg gat ggg cca aaa gtt aag caa tgg cca cta aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu aaa atc aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga 432 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly aaa att gaa aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480 Lys Ile Glu Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe gcc ata agg aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528 Ala Ile Arg Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 aga gaa ctt aat aag aga act caa gac ttt tgg gaa att caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 190 624 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 205 195 672 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 720 aag tat act gca ttt acc ata cct agt gta aat aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 230 235

att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa yta gtt atc tac caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tca gac tta gaa ata gar aag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Lys His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tya aaa tgg ggg ttt acc aca cca gac aaa aaa cat Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag acc ata aag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Thr Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atk ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly 35 40 45	144

								ctt Leu		192
								cct Pro		240
								tgc Cys 95		288
	_	_	_	_	 _	_	_	tta Leu	_	336
								gaa Glu		384
								gaa Glu		432
								gta Val		480
								gat Asp 175		528
								tta Leu		576
								gta Val		624
								ttc Phe		672
								cca Pro		720
								tca Ser 255		768
								aga Arg		816
								tat Tyr		864
								gaa Glu		912

Arg Gln His Leu Leu Lys Trp Gly Xaa Xaa Thr Pro Asp Lys Lys His 305 310 315	960
cag aaa saa cct cca ttc ctt tgg atg ggt tat gaa ctc cmt cct gat Gln Lys Xaa Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu Xaa Pro Asp 325 330 335	1008
aaa tgg aca gta caa cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln 355 360 365	1104
att tac gca ggg Ile Tyr Ala Gly 370	1116
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<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 113 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1</pre>	
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 113 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1</pre>	96
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 113 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1</pre>	96 144
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 113 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1</pre>	96 144 192

														gaa Glu		384
														gam Xaa		432
waa Xaa 145	att Ile	tca Ser	aaa Lys	mta Xaa	999 Gly 150	cct Pro	gam Xaa	wat Xaa	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cac His 195	ccg Pro	gca Ala	G1y 999	tta Leu	aaa Lys 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gtg Val	ttg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gag Glu	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	999 Gly 240	720
														tca Ser 255		768
gca Ala	ata Ile	ttc Phe	caa Gln 260	tst Xaa	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ttg Leu	912
aga Arg 305	gaa Glu	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gat Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gag Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104

att tat gca ggg Ile Tyr Ala Gly 370	1116												
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ggg gca aat aag gaa gct cta tta gac aca gga gca gat gat mca gta Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Xaa Val 20 25 30	96												
tta gaa gaa atg wat tta cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Xaa Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144												
gga att gga ggt ttt atc aaa gta agn cag tat gag cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Glu Gln Ile Pro Ile 50 60	192												
gaa atc tgt gga cat aaa gct ata ggt aca gta ttg gta ggm cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr 65 70 75 80	240												
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288												
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336												
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384												
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432												
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480												
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528												

aga gaa ctt Arg Glu Leu	aat aag Asn Lys 180	aga a Arg T	act caa Thr Glr	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtc Val	caa Gln 190	tta Leu	gga Gly	576
ata cca cat Ile Pro His 195	cct gca Pro Ala	ggg t Gly I	tta aaa Leu Lys 200	Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gtg Val	ctg Leu	624
gac gtg ggt Asp Val Gly 210		Tyr E										672
aag tat act Lys Tyr Thr 225												720
agt agg tat Ser Arg Tyr												768
gca ata ttc Ala Ile Phe												816
caa aat cca Gln Asn Pro 275												864
gga tct gac Gly Ser Asp 290		Ile d										912
aga caa cat Arg Gln His 305	ctg ttg Leu Leu	agg t Arg 1 310	tgg gga Irp Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aag Lys	aaa Lys	cat His 320	960
cag aar gaa Gln Lys Glu	cct ccg Pro Pro 325	ttc c Phe I	ctt tgg Leu Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa tgg aca Lys Trp Thr	gta cag Val Gln 340	cct a Pro I	ata gtg Ile Val	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	ags Xaa 350	ttg Leu	rct Xaa	1056
kca aat gac Xaa Asn Asp 355	ata cag Ile Gln	aag t Lys I	tta gtg Leu Val 360	Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att tac tca Ile Tyr Ser 370												1116
<210> 115 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)												
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<221> CDS <222> (298) . . . (1116) <223> Portion of HIV Reverse Transcriptase <400> 115 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gtg 96 Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val tta gaa gaa atg agt ata cca gga aaa tgg aaa cca aaa ttg ata ggg 144 Leu Glu Glu Met Ser Ile Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly gga att gga ggt ttt atc aaa gta aga cag tat gat cag gkg ccc gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Val 192 240 gaa att tgt gga cat aaa gct ata ggt mca gtw tta ata ggm cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Xaa Xaa Leu Ile Xaa Pro Thr 288 cct gcc aac ata att gga agg aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 336 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 1.05 cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gag 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa gga 432 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 170 aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga 576 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 190 624 ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 205 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttt agg 672 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 215 aaa tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 720 230 235

att aga tat o Ile Arg Tyr G	cag tat aat Gln Tyr Asn 245	gtg ctt o Val Leu 1	cca cag Pro Gln 250	gga tgg Gly Trp	aaa gga Lys Gly	tca cca Ser Pro 255	768
gca ata ttc c Ala Ile Phe G	caa tgt agt Gln Cys Ser 260	Met Thr 1	aaa ata Lys Ile 265	tta gag Leu Glu	ccc ttt Pro Phe 270	aga aaa Arg Lys	816
caa aat cca g Gln Asn Pro A 275	gac cta gtt Asp Leu Val	atc tat of Ile Tyr (	caa tac Gln Tyr	gtg gat Val Asp	gat ttg Asp Leu 285	tat gta Tyr Val	864
gga tct gac t Gly Ser Asp L 290							912
aga caa cat c Arg Gln His L 305							960
cag aaa gaa c Gln Lys Glu P							1008
aaa tgg aca g Lys Trp Thr V 3		Ile Val I					1056
gtc aat gac a Val Asn Asp I 355							1104
att tac cca g Ile Tyr Pro G 370							1116
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<220> <221> CDS <222> (1)( <223> HIV Pro							
<221> CDS <222> (298) <223> Portion		verse Tran	nscripta	ıse			
<400> 116 cct cag atc a Pro Gln Ile T 1							48
ggg cag cta a Gly Gln Leu L							96
tta gaa gaa a Leu Glu Glu I 35							144

gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aag Lys	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	ccc Pro	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	ggm Xaa	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	gtt Val 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	ctt Leu	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
						aag Lys										384
						gaa Glu 135										432
						cct Pro										480
						agt Ser										528
						act Thr										576
						tta Leu										624
						ttt Phe 215										672
						ata Ile										720
						gtg Val										768
						atg Met										816
						atc Ile										864
						999 Gly 295										912

305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
<210> 117 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
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	48
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase &lt;400&gt; 117 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly</pre>	48 96
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 117 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 117 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	96
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 117 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	96 144
<pre>&lt;223&gt; Portion of HIV Reverse Transcriptase  &lt;400&gt; 117 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly 1</pre>	96 144 192

cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	ttg Leu 140	gaa Glu	aag Lys	gaa Glu	gga Gly	432
								aat Asn								480
								aaa Lys								528
								gac Asp 185								576
								aag Lys								624
								gtt Val								672
								agt Ser								720
								cca Pro								768
								aaa Lys 265								816
								caa Gln								864
								cat His								912
aga Arg 305	gaa Glu	cat His	ctg Leu	tgg Trp	aag Lys 310	tgg Trp	G1y 999	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
								atg Met								1008
								ctg Leu 345								1056
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Ile Tyr Xaa Gly Ile

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<212> PRT
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Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys

1 5 10 15

Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys 20 25 30

Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser 35 40 45

Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys

Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys 50 55 60 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85
90
95
Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly

100 105 110
Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr

Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr 130 135 140

Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe 145 150 155 160 Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro

Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
180 185 190

Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His

Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu 210 215 220

Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr

225 230 235 240
Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp

245 250 255

Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala

Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala
260
265
270
Glv Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Glv Thr Lys Ala

Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala 275 280 285

Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala 290 295 300 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp

305 310 315 320 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln

325 330 335

Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly

340 345 350
Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu

355 360 365
Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
370 375 380

Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr 385 390 395 400
Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe

405 410 415

Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro 

 Lys
 Phe Lys
 Leu Pro
 Ile Gln Lys
 Lys
 Glu Thr Trp Glu Thr 940
 Thr Trp 940
 Thr Pro 110
 Thr 950
 Thr 940
 Thr 940